

**Figure 1A****4.1.1 Heavy Chain DNA**

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ATGGAGTTTG GGCTGAGCTG GGTTCCTC GTTGCTCTTT TAAGAGGTGT 50
CCAGTGTCAG GTGCAGCTGG TGGAGTCTGG GGGAGGCGTG GTCCAGCCTG 100
GGAGGTCCCT GAGACTCTCC TGTGTAGCGT CTGGATTAC CTTCAGTAGC 150
CATGGCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC TGGAGTGGGT 200
GGCAGTTATA TGGTATGATG GAAGAAATAA ATACTATGCA GACTCCGTGA 250
AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC GCTGTTTCTG 300
CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT ACTGTGCGAG 350
AGGAGGTCAC TTCGGTCCTT TTGACTACTG GGGCCAGGGA ACCCTGGTCA 400
CCGTCTCCTC AGCCTCCACC AAGGGCCCAT CGGTCTTCCC CCTGGCGCCC 450
TGCTCCAGGA GCACCTCCGA GAGCACAGCG GCCCTGGGCT GCCTGGTCAA 500
GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAAC TCA GGCGCTCTGA 550
CCAGCGGCGT GCACACCTTC CCAGCTGTCC TACAGTCCTC AGGACTCTAC 600
TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAACTTCG GCACCCAGAC 650
CTACACCTGC AACGTAGATC ACAAGCCCAG CAACACCAAG GTGGACAAGA 700
CAGTTGAGCG CAAATGTTGT GTCGAGTGCC CACCGTGCCC AGCACCACCT 750
GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CAAAACCCA AGGACACCCT 800
CATGATCTCC CGGACCCCTG AGGTCACGTG CGTGGTGGTG GACGTGAGCC 850
ACGAAGACCC CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG 900
CATAATGCCA AGACAAAGCC ACGGGAGGAG CAGTTCAACA GCACGTTCCG 950
TGTGGTCAGC GTCCTACCG TTGTGCACCA GGACTGGCTG AACGGCAAGG 1000
AGTACAAGTG CAAGGTCTCC AACAAAGGCC TCCCAGCCCC CATCGAGAAA 1050
ACCATCTCCA AAACCAAAGG GCAGCCCCGA GAACCACAGG TGTACACCCT 1100
GCCCCATCC CGGGAGGAGA TGACCAAGAA CCAGGTCAGC CTGACCTGCC 1150
TGGTCAAAGG CTTCTACCCC AGCGACATCG CCGTGGAGTG GGAGAGCAAT 1200
GGGCAGCCGG AGAACAATA CAAGACCACA CCTCCCATGC TGGACTCCGA 1250
CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC 1300
AGCAGGGGAA CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC 1350
CACTACACGC AGAAGAGCCT CTCCCTGTCT CCGGGTAAAT GA 1392

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(SEQ ID NO:27)

**4.1.1 Heavy Chain Protein**

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MEFGLSWVFL VALLRGVQCQ VQLVESGGGV VQPGRSLRLS CVASGFTFSS 50
HGMHWVRQAP GKGLEWVAVI WYDGRNKYYA DSVKGRFTIS RDNSKNTLFL 100
QMNSLRAEDT AVYYCARGGH FGPFDYWGQG TLVTVSSAST KGPSVFPLAP 150
CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 200
SLSSVVTGPS SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP 250
VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ FNWYVDGVEV 300
HNAKTKPREE QFNSTFRVVS VLTVVHQDWL NGKEYKCKVS NKGLPAPIEK 350
TISKTKGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN 400
GQPENNYKTT PPMLDSGDSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN 450
HYTQKSLSLS PGK 463

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(SEQ ID NO:1)

EV270264398US

**Figure 1A** (continued)**4.1.1 Kappa Chain DNA**

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ATGGAAACCC CAGCGCAGCT TCTCTTCCTC CTGCTACTCT GGCTCCCAGA 50
TACCACCGGA GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT 100
CTCCAGGGGA AAGAGCCACC CTCTCCTGCA GGGCCAGTCA GAGTATTAGC 150
AGCAGCTTCT TAGCCTGGTA CCAGCAGAGA CCTGGCCAGG CTCCCAGGCT 200
CCTCATCTAT GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA 250
GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG 300
CCTGAAGATT TTGCAGTGTA TTACTGTCAG CAGTATGGTA CCTCACCTTG 350
GACGTTCCGC CAAGGGACCA AGGTGGAAAT CAAACGAACT GTGGCTGCAC 400
CATCTGTCTT CATCTTCCCG CCATCTGATG AGCAGTTGAA ATCTGGAAct 450
GCCTCTGTTG TGTGCCTGCT GAATAACTTC TATCCCAGAG AGGCCAAAGT 500
ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC CAGGAGAGTG 550
TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTTG 600
ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT 650
CACCCATCAG GGCCTGAGCT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG 700
AGTGTTAG
708

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(SEQ ID NO:40)

**4.1.1 Kappa Chain Protein**

```

METPAQLLFL LLLWLPDTTG EIVLTQSPGT LSLSPGERAT LSCRASQSIG 50
SSFLAWYQQR PGQAPRLLIY GASSRATGIP DRFSGSGSGT DFTLTISRLE 100
PEDFAVYYCQ QYGTSPWTFG QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT 150
ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYLSSTL 200
TLISKADYEKH KVIACEVTHQ GLSSPVTKSF NRGEC
235

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(SEQ ID NO:14)

**Figure 1B****4.8.1 Heavy Chain DNA**

ATGGAGTTTG	GGCTGAGCTG	GGTTTTCTCTC	GTTGCTCTTT	TAAGAGGTGT	50
CCAGTGTCTAG	GTGCAGCTGG	TGGAGTCTGG	GGGAGGCGTG	GTCCAGCCTG	100
GGAGGTCCTT	GAGACTCTCC	TGTACAGCGT	CTGGATTAC	CTTCAGTAAC	150
TATGGCATGC	ACTGGGTCCG	CCAGGCTCCA	GGCAAGGGGC	TGGAGTGGGT	200
GGCAGTTATA	TGGTATGATG	GAAGTAATAA	ACACTATGGA	GACTCCGTGA	250
AGGGCCGATT	CACCATCTCC	AGTGACAATT	CCAAGAACAC	GCTGTATCTG	300
CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCGAG	350
AGGAGAGAGA	CTGGGGTCCT	ACTTTGACTA	CTGGGGCCAG	GGAACCCTGG	400
TCACCGTCTC	CTCAGCCTCC	ACCAAGGGCC	CATCGGTCTT	CCCCCTGGCG	450
CCCTGCTCCA	GGAGCACCTC	CGAGAGCACA	GCGGCCCTGG	GCTGCCTGGT	500
CAAGGACTAC	TTCCCCGAAC	CGGTGACGGT	GTCGTGGAAC	TCAGGCGCTC	550
TGACCAGCGG	CGTGACACAC	TTCCCAGCTG	TCCTACAGTC	CTCAGGACTC	600
TACTCCCTCA	GCAGCGTGGT	GACCGTGCCC	TCCAGCAACT	TCGGCACCCA	650
GACCTACACC	TGCAACGTAG	ATCACAAGCC	CAGCAACACC	AAGGTGGACA	700
AGACAGTTGA	GCGCAAATGT	TGTGTCTGAGT	GCCCACCGTG	CCCAGCACCA	750
CCTGTGGCAG	GACCGTCAGT	CTTCCTCTTC	CCCCCAAAC	CCAAGGACAC	800
CCTCATGATC	TCCCGGACCC	CTGAGGTCAC	GTGCGTGGTG	GTGGACGTGA	850
GCCACGAAGA	CCCCGAGGTC	CAGTTCAACT	GGTACGTGGA	CGGCGTGGAG	900
GTGCATAATG	CCAAGACAAA	GCCACGGGAG	GAGCAGTTCA	ACAGCACGTT	950
CCGTGTGGTC	AGCGTCCTCA	CCGTTGTGCA	CCAGGACTGG	CTGAACGGCA	1000
AGGAGTACAA	GTGCAAGGTC	TCCAACAAAG	GCCTCCCAGC	CCCCATCGAG	1050
AAAACCATCT	CCAAAACCAA	AGGGCAGCCC	CGAGAACCAC	AGGTGTACAC	1100
CCTGCCCCCA	TCCCGGGAGG	AGATGACCAA	GAACCAGGTC	AGCCTGACCT	1150
GCCTGGTCAA	AGGCTTCTAC	CCCAGCGACA	TCGCCGTGGA	GTGGGAGAGC	1200
AATGGGCAGC	CGGAGAACAA	CTACAAGACC	ACACCTCCCA	TGCTGGACTC	1250
CGACGGCTCC	TTCTTCCTCT	ACAGCAAGCT	CACCGTGGAC	AAGAGCAGGT	1300
GGCAGCAGGG	GAACGTCTTC	TCATGCTCCG	TGATGCATGA	GGCTCTGCAC	1350
AACCACTACA	CGCAGAAGAG	CCTCTCCCTG	TCTCCGGGTA	AATGA	1395

(SEQ ID NO:28)

**4.8.1 Heavy Chain Protein**

MEFGLSWVFL	VALLRGVQCQ	VQLVESGGGV	VQPGRSLRLS	CTASGFTFSN	50
YGMHWVRQAP	GKGLEWVAVI	WYDGSNKHYG	DSVKGRFTIS	SDNSKNTLYL	100
QMNSLRAEDT	AVYYCARGER	LGSYFDYWGQ	GTLVTVSSAS	TKGPSVFPLA	150
PCSRSTSEST	AALGCLVKDY	FPEPVTVSWN	SGALTSGVHT	FPAVLQSSGL	200
YSLSSVVTVP	SSNFGTQTYT	CNVDHKPSNT	KVDKTKVERKC	CVECPPCPAP	250
PVAGPSVFLF	PPKPKDTLMI	SRTPEVTCVV	VDVSHEDPEV	QFNWYVDGVE	300
VHNAKTKPRE	EQFNSTFRVV	SVLTVVHQDW	LNGKEYKCKV	SNKGLPAPIE	350
KTISKTKGQP	REPQVYTLPP	SREEMTKNQV	SLTCLVKGFY	PSDIAVEWES	400
NGQPENNYKT	TPPMLDSDGS	FFLYSKLTVD	KSRWQQGNVF	SCSVMHEALH	450
NHYTQKSLSL	SPGK				464

(SEQ ID NO:2)

**Figure 1B** (continued)**4.8.1 Kappa Chain DNA**

```

ATGGAAACCC CAGCGCAGCT TCTCTTCCTC CTGCTACTCT GGCTCCCAGA 50
TACCACCGGA GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT 100
CTCCAGGGGA AAGAGCCACC CTCTCCTGCA GGACCAGTGT TAGCAGCAGT 150
TACTTAGCCT GGTACCAGCA GAAACCTGGC CAGGCTCCCA GGCTCCTCAT 200
CTATGGTGCA TCCAGCAGGG CCACTGGCAT CCCAGACAGG TTCAGTGGCA 250
GTGGGTCTGG GACAGACTTC ACTCTCACCA TCAGCAGACT GGAGCCTGAA 300
GATTTTGCAG TCTATTACTG TCAGCAGTAT GGCATCTCAC CCTTCACTTT 350
CGGCGGAGGG ACCAAGGTGG AGATCAAGCG AACTGTGGCT GCACCATCTG 400
TCTTCATCTT CCCGCCATCT GATGAGCAGT TGAAATCTGG AACTGCCTCT 450
GTTGTGTGCC TGCTGAATAA CTTCTATCCC AGAGAGGCCA AAGTACAGTG 500
GAAGGTGGAT AACGCCCTCC AATCGGGTAA CTCCAGGAG AGTGTACAG 550
AGCAGGACAG CAAGGACAGC ACCTACAGCC TCAGCAGCAC CCTGACGCTG 600
AGCAAAGCAG ACTACGAGAA ACACAAAGTC TACGCCTGCG AAGTCACCCA 650
TCAGGGCCTG AGCTCGCCCG TCACAAAGAG CTTCAACAGG GGAGAGTGTT 700
AG
702

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(SEQ ID NO:41)

**4.8.1 Kappa Chain Protein**

```

METPAQLLFL LLLWLPDTTG EIVLTQSPGT LSLSPGERAT LSCRTSVSSS 50
YLAWYQQKPG QAPRLLIYGA SSRATGIPDR FSGSGSGTDF TLTISRLEPE 100
DFAVYYCQQY GISPFTFGGG TKVEIKRTVA APSVFIFPPS DEQLKSGTAS 150
VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL 200
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC 233

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(SEQ ID NO:15)

## Figure 1C

### 4.14.3 Heavy Chain DNA

```

CCTGGGAGGT CCCTGAGACT CTCCTGTGCA GCGTCTGGAT TCACCTTCAG 50
TAGTCATGGC ATCCACTGGG TCCGCCAGGC TCCAGGCAAG GGGCTGGAGT 100
GGGTGGCAGT TATATGGTAT GATGGAAGAA ATAAAGACTA TGCAGACTCC 150
GTGAAGGGCC GATTACCAT CTCCAGAGAC AATTCCAAGA AGACGCTGTA 200
TTTGCAAATG AACAGCCTGA GAGCCGAGGA CACGGCTGTG TATTACTGTG 250
CGAGAGTGGC CCCACTGGGG CCACTTGACT ACTGGGGCCA GGAACCCTG 300
GTCACCGTCT CCTCAGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 350
GCCCTGCTCC AGGAGCACCT CCGAGAGCAC AGCGGCCCTG GGCTGCCTGG 400
TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCT 450
CTGACCAGCG GCGTGCACAC CTTCCCAGCT GTCCTACAG 489

```

(SEQ ID NO:29)

### 4.14.3 Heavy Chain Protein

```

PGRSLRLSCA ASGFTFSSHG IHWVRQAPGK GLEWVAVIWY DGRNKDYADS 50
VKGRFTISRQ NSKKTLYLQM NSLRAEDTAV YYCARVAPLG PLDYWGQGT 100
VTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA 150
LTSGVHTFPA VLQ 163

```

(SEQ ID NO:3)

### 4.14.3 Kappa Chain DNA

```

GGCACCTGT CTTTGTCTCC AGGGGAAAGA GCCACCCTCT CCTGCAGGGC 50
CAGTCAGAGT GTCAGCAGCT ACTTAGCCTG GTACCAGCAG AACCTGGCC 100
AGGCTCCCAG ACTCCTCATC TATGGTGCAT CCAGCAGGGC CACTGGCATC 150
CCAGACAGGT TCAGTGGCAG TGGGTCTGGG ACAGACTTCA CTCTACCAT 200
CAGCAGACTG GAGCCTGAGG ATTTTGCAGT GTATTACTGT CAGCAGTATG 250
GTAGGTCACC ATTCACCTTC GGCCCTGGGA CCAAAGTGGA TATCAAGCGA 300
ACTGTGGCTG CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT 350
GAAATCTGGA ACTGCCTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA 400
GAGAGGCCAA AGTACAG 417

```

(SEQ ID NO:42)

### 4.14.3 Kappa Chain Protein

```

GTLSLSPGER ATLSCRASQS VSSYLAWYQQ KPGQAPRLLI YGASSRATGI 50
PDRFSGSGSG TDFTLTISRL EPEDFAVYYC QQYGRSPFTF GPGTKVDIKR 100
TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ 139

```

(SEQ ID NO:16)

**Figure 1D****6.1.1 Heavy Chain DNA**

ATGGAGTTTG	GGCTGAGCTG	GGTTTTCTC	GTTGCTCTTT	TAAGAGGTGT	50
CCAGTGTCAG	GTGCAGCTGG	TGGAGTCTGG	GGGAGGCGTG	GTCGAGCCTG	100
GGAGGTCCCT	GAGACTCTCC	TGTACAGCGT	CTGGATTAC	CTTCAGTAGT	150
TATGGCATGC	ACTGGGTCCG	CCAGGCTCCA	GGCAAGGGGC	TGGAGTGGGT	200
GGCAGTTATA	TGGTATGATG	GAAGCAATAA	ACACTATGCA	GACTCCGCGA	250
AGGGCCGATT	CACCATCTCC	AGAGACAATT	CCAAGAACAC	GCTGTATCTG	300
CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCGAG	350
AGCCGGACTG	CTGGGTTACT	TTGACTACTG	GGGCCAGGGA	ACCCTGGTCA	400
CCGTCTCCTC	AGCCTCCACC	AAGGGCCCAT	CGGTCTTCCC	CCTGGCGCCC	450
TGCTCCAGGA	GCACCTCCGA	GAGCACAGCG	GCCCTGGGCT	GCCTGGTCAA	500
GGACTACTTC	CCCGAACCGG	TGACGGTGTC	GTGGAACCTCA	GGCGCTCTGA	550
CCAGCGGCGT	GCACACCTTC	CCAGCTGTCC	TACAGTCCTC	AGGACTCTAC	600
TCCCTCAGCA	GCGTGGTGAC	CGTGCCCTCC	AGCAACTTCG	GCACCCAGAC	650
CTACACCTGC	AACGTAGATC	ACAAGCCCAG	CAACACCAAG	GTGGACAAGA	700
CAGTTGAGCG	CAAATGTTGT	GTCGAGTGCC	CACCGTGCCC	AGCACCACCT	750
GTGGCAGGAC	CGTCAGTCTT	CCTCTTCCCC	CCAAAACCCA	AGGACACCCT	800
CATGATCTCC	CGGACCCCTG	AGGTCACGTG	CGTGGTGGTG	GACGTGAGCC	850
ACGAAGACCC	CGAGGTCCAG	TTCAACTGGT	ACGTGGACGG	CGTGGAGGTG	900
CATAATGCCA	AGACAAAGCC	ACGGGAGGAG	CAGTTCAACA	GCACGTTCCG	950
TGTGGTCAGC	GTCCTCACCG	TTGTGCACCA	GGACTGGCTG	AACGGCAAGG	1000
AGTACAAGTG	CAAGGTCTCC	AACAAAGGCC	TCCCAGCCCC	CATCGAGAAA	1050
ACCATCTCCA	AAACCAAAGG	GCAGCCCCGA	GAACCACAGG	TGTACACCCT	1100
GCCCCCATCC	CGGGAGGAGA	TGACCAAGAA	CCAGGTCAGC	CTGACCTGCC	1150
TGGTCAAAGG	CTTCTACCCC	AGCGACATCG	CCGTGGAGTG	GGAGAGCAAT	1200
GGGCAGCCGG	AGAACAATA	CAAGACCACA	CCTCCCATGC	TGGACTCCGA	1250
CGGCTCCTTC	TTCCTCTACA	GCAAGCTCAC	CGTGGACAAG	AGCAGGTGGC	1300
AGCAGGGGAA	CGTCTTCTCA	TGCTCCGTGA	TGCATGAGGC	TCTGCACAAC	1350
CACTACACGC	AGAAGAGCCT	CTCCCTGTCT	CCGGGTAAAT	GA	1392

(SEQ ID NO:30)

**6.1.1 Heavy Chain Protein**

MEFGLSWVFL	VALLRGVQCQ	VQLVESGGGV	VEPGRSLRLS	CTASGFTFSS	50
YGMHWVRQAP	GKGLEWVAVI	WYDGSNKHYA	DSAKGRFTIS	RDNSKNTLYL	100
QMNSLRAEDT	AVYYCARAGL	LGYFDYWQGG	TLVTVSSAST	KGPSVFPLAP	150
CSRSTSESTA	ALGCLVKDYF	PEPVTVSWNS	GALTSGVHTF	PAVLQSSGLY	200
SLSSVVTVPS	SNFGTQTYTC	NVDHKPSNTK	VDKTVERKCC	VECPPCPAPP	250
VAGPSVFLFP	PKPKDTLMIS	RTPEVTCVVV	DVSHEDPEVQ	FNWYVDGVEV	300
HNAKTKPREE	QFNSTFRVVS	VLTVVHQDWL	NGKEYKCKVS	NKGLPAPIEK	350
TISKTKGQPR	EPQVYTLPPS	REEMTKNQVS	LTCLVKGFYP	SDIAVEWESN	400
GQPENNYKTT	PPMLDSGGSF	FLYSKLTVDK	SRWQQGNVFS	CSVMHEALHN	450
HYTQKSLSL	PGK				463

(SEQ ID NO:4)

**Figure 1D** (continued)**6.1.1 Kappa Chain DNA**

<u>ATGGAAACCC</u>	<u>CAGCGCAGCT</u>	<u>TCTCTTCCTC</u>	<u>CTGCTACTCT</u>	<u>GGCTCCCAGA</u>	50
TACCACCGGA	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	100
CTCCAGGGGA	AAGAGCCACC	CTCTCCTGTA	GGGCCAGTCA	AAGTGTTAGC	150
AGCTACTTAG	CCTGGTACCA	ACAGAAACCT	GGCCAGGCTC	CCAGGCCCCCT	200
CATCTATGGT	GTATCCAGCA	GGGCCACTGG	CATCCCAGAC	AGGTTCAGTG	250
GCAGTGGGTC	TGGGACAGAC	TTCACTCTCA	CCATCAGCAG	ACTGGAGCCT	300
GAAGATTTTG	CAGTGTATTA	CTGTCAGCAG	TATGGTATCT	CACCATTAC	350
TTTCGGCCCT	GGGACCAAAG	TGGATATCAA	ACGAACTGTG	GCTGCACCAT	400
CTGTCTTCAT	CTTCCCGCCA	TCTGATGAGC	AGTTGAAATC	TGGAAGTACC	450
TCTGTTGTGT	GCCTGCTGAA	TAACCTCTAT	CCCAGAGAGG	CCAAAGTACA	500
GTGGAAGGTG	GATAACGCCC	TCCAATCGGG	TAACCTCCAG	GAGAGTGTCA	550
CAGAGCAGGA	CAGCAAGGAC	AGCACCTACA	GCCTCAGCAG	CACCCTGACG	600
CTGAGCAAAG	CAGACTACGA	GAAACACAAA	GTCTACGCCT	GCGAAGTCAC	650
CCATCAGGGC	CTGAGCTCGC	CCGTCACAAA	GAGCTTCAAC	AGGGGAGAGT	700
GTTAG					705

(SEQ ID NO:43)

**6.1.1 Kappa Chain Protein**

METPAQLLFL	LLLWLPDTTG	EIVLTQSPGT	LSLSPGERAT	LSCRASQSVS	50
SYLAWYQQKP	GOAPRPLIYG	VSSRATGIPD	RFSGSGSGTD	FTLTISRLEP	100
EDFAVYYCQQ	YGISPFTFGP	GTKVDIKRTV	AAPSVFIFPP	SDEQLKSGTA	150
SVVCLLNIFY	PREAKVQWKV	DNALQSGNSQ	ESVTEQDSKD	STYSLSSTLT	200
LSKADYEKHK	VYACEVTHQG	LSSPVTKSFN	RGEC		234

(SEQ ID NO:17)

**Figure 1E****3.1.1 Heavy Chain DNA**

```

GGCGTGGTCC AGCCTGGGAG GTCCCTGAGA CTCTCCTGTG CAGCGTCTGG 50
ATTCACCTTC AGTAGCTATG GCATGCACTG GGTCCGCCAG GCTCCAGGCA 100
AGGGGCTGGA GTGGGTGGCA GTTATATGGT ATGATGGAAG TAATAAATAC 150
TATGCAGACT CCGTGAAGGG CCGATTCAAC ATCTCCAGAG ACAATTCCAA 200
GAACACGCTG TATCTGCAAA TGAACAGCCT GAGAGCCGAG GACACGGCTG 250
TGTATTACTG TGCAGAGAGG GCCCGTATAA TAACCCCTTG TATGGACGTC 300
TGGGGCCAAG GGACCACGGT CACCGTCTCC TCAGCCTCCA CCAAGGGCCC 350
ATCGGTCTTC CCCCTGGCGC CCTGCTCCAG GAGCACCTCC GAGAGCACAG 400
CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 450
TCGTGGAAC T CAGGCGCTCT GACCAGCGGC GTGCACACCT TCCAGCTGT 500
CCTACAG 507

```

(SEQ ID NO:31)

**3.1.1 Heavy Chain Protein**

```

GVVQPGRSLR LSCAASGFTF SSYGMHWVRQ APGKGLEWVA VIWYDGSNKY 50
YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARG ARIITPCMDV 100
WGQGTITVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV 150
SWNSGALTSG VHTFPAVLQ 169

```

(SEQ ID NO:5)

**3.1.1 Kappa Chain DNA**

```

CAGTCTCCAT CCTCCCTGTC TGCATCTGTA GGAGACAGAG TCACCATCAC 50
TTGCCGGGCA AGTCAGAGCA TTAACACCTA TTTAATTTGG TATCAGCAGA 100
AACCAGGGAA AGCCCCTAAC TTCCTGATCT CTGCTACATC CATTTTGCAA 150
AGTGGGGTCC CATCAAGGTT CCGTGGCAGT GGCTCTGGGA CAAATTTTCA 200
TCTCACCATC AACAGTCTTC ATCCTGAAGA TTTTGCAACT TACTACTGTC 250
AACAGAGTTA CAGTACCCCA TTCACTTTTCG GCCCTGGGAC CAAAGTGGAT 300
ATCAAACGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA 350
TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT 400
TCTATCCAG AGAGGCCAAA GTACAGTGGG AGGTGGATAA CGCCCTCCAA 450
TCGGGTAA 458

```

(SEQ ID NO:44)

**3.1.1 Kappa Chain Protein**

```

QSPSSLSASV GDRVITTCRA SQSINTYLIW YQQKPGKAPN FLISATSILQ 50
SGVPSRFRGS GSGTNFTLTI NSLHPEDFAT YYCQQSYSTP FTFGPGTKVD 100
IKRTVAAPSV FIFPPSDEQL KSGTASVCL LNNFYPRK VQWKVDNALQ 150
SG 152

```

(SEQ ID NO:18)



**Figure 1F****4.10.2 Heavy Chain DNA**

```

GGCGTGGTCC AGCCTGGGAG GTCCCTGAGA CTCTCCTGTG TAGCGTCTGG 50
ATTCATCTTC AGTAGTCATG GCATCCACTG GGTCCGCCAG GCTCCAGGCA 100
AGGGGCTGGA GTGGGTGGCA GTTATATGGT ATGATGGAAG AAATAAAGAC 150
TATGCAGACT CCGTGAAGGG CCGATTCAAC ATCTCCAGAG ACAATTCCAA 200
GAACACGCTG TATTTGCAAA TGAACAGCCT GAGAGCCGAG GACACGGCTG 250
TGTATTACTG TGCAGAGAGT GCCCCTACTG GGCCACTTGA CTACTGGGGC 300
CAGGGAACCC TGGTCACCGT CTCCTCAGCC TCCACCAAGG GCCCATCGGT 350
CTTCCCCCTG GCGCCCTGCT CCAGGAGCAC CTCCGAGAGC ACAGCGGCC 400
TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 450
AACTCAGGCG CTCTGACCAG CGGCGTGCAC ACCTTCCCAG CTGTCCTACA 500
G 501

```

(SEQ ID NO:32)

**4.10.2 Heavy Chain Protein**

```

GVVQPGRSLR LSCVASGFIF SSHGIHWVRQ APGKGLEWVA VIWYDGRNKD 50
YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARV APLGPLDYWG 100
QGTLVTVSSA STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW 150
NSGALTSGVH TFPVLQ 167

```

(SEQ ID NO:6)

**4.10.2 Kappa Chain DNA**

```

TCTCCAGGCA CCCTGTCTTT GTCTCCAGGG GAAAGAGCCA CCCTCTCCTG 50
CAGGGCCAGT CAGAGTATTA GCAGCAATTT CTTAGCCTGG TACCAGCAGA 100
AACCTGGCCA GGCTCCCAGG CTCCTCATCT ATCGTCCATC CAGCAGGGCC 150
ACTGGCATCC CAGACAGTTT CAGTGGCAGT GGGTCTGGGA CAGACTTCAC 200
TCTCACCATC AGCAGACTGG AGCCTGAGGA TTTTGCATTA TATTACTGTC 250
AGCAGTATGG TACGTCACCA TTCACTTTCG GCCCTGGGAC CAAAGTGGAT 300
ATCAAGCGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA 350
TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT 400
TCTATCCCAG AGAGGCCAAA GTACAG 426

```

(SEQ ID NO:45)

**4.10.2 Kappa Chain Protein**

```

SPGTLSLSPG ERATLSCRAS QSISSNFLAW YQKPGQAPR LLIYRPSSRA 50
TGIPDSFSGS GSGTDFTLTI SRLEPEDFAL YYCQYGTSP FTFGPGTKVD 100
IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK VQ 142

```

(SEQ ID NO:19)

**Figure 1G****2.1.3 Heavy Chain DNA**

TCGGGCCCCAG	GACTGGTGAA	GCCTTCACAG	ATCCTGTCCC	TCACCTGCAC	50
TGTCTCTGGT	GGCTCCATCA	GCAGTGGTGG	TCACTACTGG	AGCTGGATCC	100
GCCAGCACCC	AGGGAAGGGC	CTGGAGTGGA	TTGGGTACAT	CTATTACATT	150
GGGAACACCT	ACTACAACCC	GTCCCTCAAG	AGTCGAGTTA	CCATATCAGT	200
AGACACGTCT	AAGAACCAGT	TCTCCCTGAA	GCTGAGCTCT	GTGACTGCCG	250
CGGACACGGC	CGTGTATTAT	TGTGCGAGAG	ATAGTGGGGA	CTACTACGGT	300
ATAGACGTCT	GGGGCCAAGG	GACCACGGTC	ACCGTCTCCT	CAGCTTCCAC	350
CAAGGGCCCA	TCCGTCTTCC	CCCTGGCGCC	CTGCTCCAGG	AGCACCTCCG	400
AGAGCACAGC	CGCCCTGGGC	TGCCTGGTCA	AGGACTACTT	CCCCGAACCG	450
GTGACGGTGT	CGTGGAATC	AGGCGCCCTG	ACCAGCGGCG	TGCACACCTT	500
CCCGGCTGTC	CTACAA				516

(SEQ ID NO:33)

**2.1.3 Heavy Chain Protein**

SGPGLVKPSQ	ILSLTCTVSG	GSISSGGHYW	SWIRQHPGKG	LEWIGYIYYI	50
GNTYYNPSLK	SRVTISVDTS	KNQFSLKLSS	VTAADTAVYY	CARDSGDYYG	100
IDVWGQGTTV	TVSSASTKGP	SVFPLAPCSR	STSESTAALG	CLVKDYFPEP	150
VTVSWNSGAL	TSGVHTFPAV	LQ			172

(SEQ ID NO:7)

**2.1.3 Kappa Chain DNA**

TCTCCAGACT	TTCAGTCTGT	GACTCCAAAG	GAGAAAGTCA	CCATCACCTG	50
CCGGGCCAGT	CAGAGCATTG	GTAGTAGCTT	ACATTGGTAT	CAGCAGAAAC	100
CAGATCAGTC	TCCAAAGCTC	CTCATCAAGT	ATGCTTCCCA	GTCCTTCTCT	150
GGGGTCCCCT	CGAGGTTTCA	TGGCAGTGGA	TCTGGGACAG	ATTTACCCCT	200
CACCATCAAT	AGCCTGGAAG	CTGAAGATGC	TGCAACGTAT	TACTGTCATC	250
AGAGTAGTAG	TTTACCGCTC	ACTTTCGGCG	GAGGGACCAA	GGTGGAGATC	300
AAACGAACTG	TGGCTGCACC	ATCTGTCTTC	ATCTTCCCCG	CATCTGATGA	350
GCAGTTGAAA	TCTGGAAGT	CCTCTGTTGT	GTGCCTGCTG	AATAACTTCT	400
ATCCCAGAGA	GGCCAAAGTA	CAGTGGAAGG	TGGATAACGC	CCTCCAATCG	450
GGTAACTCCC	AGGAG				465

(SEQ ID NO:46)

**2.1.3 Kappa Chain Protein**

SPDFQSVTPK	EKVTITCRAS	QSIGSSLHWY	QOKPDQSPKL	LIKYASQSFS	50
GVPSRFSGSG	SGTDFTLTIN	SLEAEDAATY	YCHQSSSLPL	TFGGGTVKVEI	100
KRTVAAPSVF	IFPPSDEQLK	SGTASVCLL	NNFYPREAKV	QWKVDNALQS	150
GNSQE					155

(SEQ ID NO:20)

**Figure 1H****4.13.1 Heavy Chain DNA**

```

CCTGGGAGGT CCCTGAGACT CTCCTGTGCA GCGTCTGGAT TCACCTTCAG 50
TAGTCATGGC ATCCACTGGG TCCGCCAGGC TCCAGGCAAG GGGCTGGAGT 100
GGGTGGCAGT TATATGGTAT GATGGAAGAA ATAAAGACTA TGCAGACTCC 150
GTGAAGGGCC GATTCACCAT CTCCAGAGAC AATTCCAAGA ACACGCTGTA 200
TTTGCAAATG AACAGCCTGA GAGCCGAGGA CACGGCTGTG TATTACTGTG 250
CGAGAGTGGC CCCACTGGGG CCACTTGACT ACTGGGGCCA GGAACCCCTG 300
GTCACCGTCT CCTCAGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 350
GCCCTGCTCC AGGAGCACCT CCGAGAGCAC AGCGGCCCTG GGCTGCCTGG 400
TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCT 450
CTGACCAGC                                     459

```

(SEQ ID NO:34)

**4.13.1 Heavy Chain Protein**

```

PGRSLRLSCA ASGFTFSSHG IHWVRQAPGK GLEWVAVIWY DGRNKDYADS 50
VKGRFTISR D NSKNTLYLQM NSLRAEDTAV YYCARVAPLG PLDYWGQGT 100
VTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA 150
LTS                                     153

```

(SEQ ID NO:8)

**4.13.1 Kappa Chain DNA**

```

CAGTCTCCAG GCACCCTGTC TTTGTCTCCA GGGGAAAGAG CCACCCTCTC 50
CTGCAGGGCC AGTCAGAGTG TCAGCAGCTA CTTAGCCTGG TACCAGCAGA 100
AACCTGGCCA GGCTCCCAGG CTCCTCATCT ATGGTGCATC CAGCAGGGCC 150
ACTGGCATCC CAGACAGGTT CAGTGGCAGT GGGTCTGGGA CAGACTTCAC 200
TCTCACCATC AGCAGACTGG AGCCTGAGGA TTTTGCAGTG TATTACTGTC 250
AACAGTATGG TAGGTCACCA TTCACTTTCG GCCCTGGGAC CAAAGTAGAT 300
ATCAAGCGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA 350
TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT 400
TCTATCCCAG AGAGGCCAAA GTACAGTGGA AAGGTGGATA 440

```

(SEQ ID NO:47)

**4.13.1 Kappa Chain Protein**

```

QSPGTLSSLSP GERATLSCRA SQSVSSYLAW YQKPGQAPR LLIYGASSRA 50
TGIPDRFSGS GSGTDFTLTI SRLEPEDFAV YYCQYGRSP FTFGPGTKVD 100
IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK VQWKGG 146

```

(SEQ ID NO:21)

**Figure 1l****11.2.1 Heavy Chain DNA**

GGCGTGGTCC	AGCCTGGGAG	GTCCCTGAGA	CTCTCCTGTG	CAGCGTCTGG	50
ATTCACCTTC	AGTAGCTATG	GCATGCACTG	GGTCCGCCAG	GCTCCAGGCA	100
AGGGGCTGGA	GTGGGTGGCA	GTTATATGGT	ATGATGGAAG	TAATAAATAC	150
TATGCAGACT	CCGTGAAGGG	CCGATTCACT	ATCTCCAGAG	ACAATTCCAA	200
GAACACGCTG	TATCTGCAAA	TGAACAGCCT	GAGAGCCGAG	GACACGGCTG	250
TGTATTACTG	TGCGAGAGAT	CCGAGGGGAG	CTACCCTTTA	CTACTACTAC	300
TACCGGTKGG	ACGTCTGGGG	CCAAGGGACC	ACGGTCACCG	TCTCCTCAGC	350
CTCCACCAAG	GGCCCATCGG	TCTTCCCCCT	GGCGCCCTGC	TCCAGGAGCA	400
CCTCCGAGAG	CACAGCGGCC	CTGGGCTGCC	TGGTCAAGGA	CTACTTCCCC	450
GAACCGGTGA	CGGTGTCGTG	GAACTCAGGC	GCTCTGACCA	GCGGCGTGCA	500
CAC					503

(SEQ ID NO:35)

**11.2.1 Heavy Chain Protein**

GVVQPGRSLR	LSCAASGFTF	SSYGMHWVRQ	APGKGLEWVA	VIWYDGSNKY	50
YADSVKGRFT	ISRDN SKNTL	YLQMN SLRAE	DTAVYYCARD	PRGATLYYYY	100
YRXDVWGQGT	TVTVSSASTK	GPSVFPLAPC	SRSTSESTAA	LGCLVKDYFP	150
EPVTVSWNSG	ALTSGVH				167

(SEQ ID NO:9)

**11.2.1 Kappa Chain DNA**

CCATCCTCCC	TGTCTGCATC	TGTAGGAGAC	AGAGTCACCA	TCACTTGCCG	50
GGCAAGTCAG	AGCATTAACA	GCTATTTAGA	TTGGTATCAG	CAGAAACCAG	100
GGAAAGCCCC	TAAACTCCTG	ATCTATGCTG	CATCCAGTTT	GCAAAGTGGG	150
GTCCCATCAA	GGTTCAGTGG	CAGTGGATCT	GGGACAGATT	TCACTCTCAC	200
CATCAGCAGT	CTGCAACCTG	AAGATTTTGC	AACTTACTAC	TGTCAACAGT	250
ATTACAGTAC	TCCATTCACT	TTCGGCCCTG	GGACCAAAGT	GGAAATCAAA	300
CGAACTGTGG	CTGCACCATC	TGTCTTCATC	TTCCCGCCAT	CTGATGAGCA	350
GTTGAAATCT	GGAAGTGCCT	CTGTTGTGTG	CCTGCTGAAT	AACTTCTATC	400
CCAGAGAGGC	CAAAGTA				417

(SEQ ID NO:48)

**11.2.1 Kappa Chain Protein**

PSSLSASVGD	RVTITCRASQ	SINSYLDWYQ	QKPGKAPKLL	IYAASSLQSG	50
VPSRFSGSGS	GTDFTLTISS	LQPEDFATYY	CQQYYSTPFT	FPGPTKVEIK	100
RTVAAPSVFI	FPPSDEQLKS	GTASVVCLLN	NFYPPREKAV		139

(SEQ ID NO:22)

**Figure 1J****11.6.1 Heavy Chain DNA**

```

GGCGTGGTCC AGCCTGGGAG GTCCCTGAGA CTCTCCTGTG CAGCGTCTGG 50
ATTCACCTTC AGTAGCTATG GCATGCACTG GGTCCGCCAG GCTCCAGGCA 100
AGGGGCTGGA GTGGGTGGCA GTTATATGGT ATGATGGAAG TCATAAATAC 150
TATGCAGACT CCGTGAAGGG CCGATTCAAC ATCTCCAGAG ACAATTCCAA 200
GAACACGCTG TATCTGCAA TGAACAGCCT GAGAGCCGAG GACACGGCTG 250
TGTATTACTG TGCAGAGAGG GCTGTAGTAG TACCAGCTGC TATGGACGTC 300
TGGGGCCAAG GGACCACGGT CACCGTCTCC TCAGCCTCCA CCAAGGGCCC 350
ATCGGTCTTC CCCCTGGCGC CCTGCTCCAG GAGCACCTCC GAGAGCACAG 400
CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 450
T

```

(SEQ ID NO:36)

**11.6.1 Heavy Chain Protein**

```

GVVQGRSLR LSCAASGFTF SSYGMHWVRQ APGKGLEWVA VIWYDGS HKY 50
YADSVKGRFT ISRDNSKNTL YLQMSNLRAE DTAVYYCARG AVVVPAAMDV 100
WGQGT TVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV 150
S

```

(SEQ ID NO:10)

**11.6.1 Kappa Chain DNA**

```

ACCCAGTCTC CATCCTCCCT GTCTGCATCT GTAGGAGACA GAGTCACCAT 50
CACTTGCCGG GCAAGTCAGA ACATTAGCAG GTATTTAAAT TGGTATCAAC 100
AGAAACCAGG GAAAGCCCCT AAGTTCCTGA TCTATGTTGC ATCTATTTTG 150
CAAAGTGGGG TCCCATCAGG GTTCAGTGCC AGTGGATCTG GGCCAGATTT 200
CACTCTNACC ATCAGCAGTC TGCAACCTGA AGATTTTGCA ACTTACTACT 250
GTCAACAGAG TTACAGTACC CCATTCACTT TCGGCCCTGG GACCAAAGTG 300
GATATCAAAC GAACTGTGGC TGCACCATCT GTCTTCATCT TCCCGCCATC 350
TGATGAGCAG TTGAAATCTG GAACTGCCTC TGTTGTGTGC CTGCTGAATA 400
AC

```

(SEQ ID NO:49)

**11.6.1 Kappa Chain Protein**

```

TQSPSSLSAS VGDRVITTCR ASQNISRYLN WYQQKPGKAP KFLIYVASIL 50
QSGVPSGFS SSGSPDFTLT ISSLPEDFA TYYCQQSYST PFTFGPGTKV 100
DIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNN

```

(SEQ ID NO:23)

**Figure 1K****11.7.1 Heavy Chain DNA**

```

GTGGTCCAGC CTGGGAGGTC CCTGAGACTC TCCTGTGCAG CGTCTGGATT 50
CACCTTCAGT AGCNGTGGCA TGCAGTGGGT CCGCCAGGCT CCAGGCAAGG 100
GGCTGGAGTG GGTGGCAGTT ATATGGTCTG ATGGAAGTCA TAAATACTAT 150
GCAGACTCCG TGAAGGGCCG ATTCACCATC TCCAGAGACA ATTCCAAGAA 200
CACGCTGTAT CTGCAAATGA ACAGCCTGAG AGCCGAGGAC ACGGCTGTGT 250
ATTACTGTGC GAGAGGAACT ATGATAGTAG TGGGTACCCT TGACTACTGG 300
GGCCAGGGAA CCCTGGTCAC CGTCTCCTCA GCCTCCACCA AGGGCCCATC 350
GGTCTTCCCC CTGGCGCCCT GCTCCAGGAG CACCTCCGAG AGCACAGCGG 400
CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCG 438

```

(SEQ ID NO:37)

**11.7.1 Heavy Chain Protein**

```

VVQPGRSLRL SCAASGFTFS SXGMHWVRQA PGKGLEWVAV IWSDGSHKYY 50
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARGT MIVVGTLDYW 100
GQGTLLTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEP 146

```

(SEQ ID NO:11)

**11.7.1 Kappa Chain DNA**

```

ACCCAGTCTC CATCCTCCCT GTCTGCATCT GTAGGAGACA GAGTCACCAT 50
CACTTGCCGG GCAAGTCAGA GCATTTGCAA CTATTTAAAT TGGTATCAGC 100
AGAAACCAGG AAAAGCCCCCT AGGGTCCTGA TCTATGCTGC ATCCAGTTTG 150
CAAGGTGGGG TCCCGTCAAG GTTCAGTGGC AGTGGATCTG GGACAGATTG 200
CACTCTCACC ATCAGCAGTC TGCAACCTGA AGATTTTGCA ACTTACTACT 250
GTCAACAGAG TTACACTACC CCATTCACTT TCGGCCCTGG GACCAGAGTG 300
GATATCGAAC GAACTGTGGC TGCACCATCT GTCTTCATCT TCCCGCCATC 350
TGATGAGCAG TTGAAATCTG GAACTGCCTC TGTTGTGTGC CTGCTGAATA 400
ACTTCTATCC CAGAGAGGCC AAAGTACAGT GGAAGGTGGA TAACGCCTAT 450
T

```

(SEQ ID NO:50)

**11.7.1 Kappa Chain Protein**

```

TQSPSSLSAS VGDRVITICR ASQSICNYLN WYQQKPGKAP RVLIYAASSL 50
QGGVPSRFSG SGSGIDCTLT ISSLPEDFA TYYCQQSYIT PFTFGPGTRV 100
DIERTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA KVQWKVDNAY 150

```

(SEQ ID NO:24)

**Figure 1L****12.3.1.1 Heavy Chain DNA**

TCCTGTGCAG	CGTCTGGATT	CACCTTCAGT	TACTATGGCG	TCTGGGGGAG	50
GCGTGGTCCA	GCCTGGGAGG	TCCCTGAGAC	TCTCCTGTGC	AGCGTCTGGA	100
TTCACCTTCA	GTAGCTATGG	CGTGCACTGG	GTCCGCCAGG	CTCCAGGCAA	150
GGGGCTGGAG	TGGGTGGCAG	TTATATGGTA	TGATGGAAGT	AATAAATACT	200
ATGCAGACTC	CGTGAAGGGC	CGATTACCA	TCTCCAGAGA	CAATTCCAAG	250
AGCACGCTGT	ATCTGCAAA	GAACAGCCTG	AGAGCCGAGG	ACACGGCTGT	300
GTATTATTGT	GCGAGAGACT	CGTATTACGA	TTTTTGGAGT	GGTCGGGGCG	350
GTATGGACGT	CTGGGGCCAA	GGGACCACGG	TCACCGTCTC	CTCAGCCTCC	400
ACCAAGGGCC	CATCGGTCTT	CCCCCTGGCG	CCCTGCTCCA	GGAGCACCTC	450
CGAGAGCACA	GCGGCCCTGG	GCTGCCTGGT	CAAGGACTAC	TTCCCCGAAC	500
CGGTGACGGT	GTCGTGGAAC	TCAGGCGCTC	TGACCAGCGG	CGTGCACACC	550
TTCCCAGCTG	TC				562

(SEQ ID NO:38)

**12.3.1.1 Heavy Chain Protein**

SGGGVVQPGR	SLRLSCAASG	FTFSSYGVHW	VRQAPGKGLE	WVAVIWDGGS	50
NKYYADSVKG	RFTISRDNK	STLYLQMNSL	RAEDTAVYYC	ARDSYYDFWS	100
GRGGMVDVWQ	GTTVTVSSAS	TKGPSVFPLA	PCSRSTSEST	AALGCLVKDY	150
FPEPVTVSWN	SGALTSGVHT	FPAV			174

(SEQ ID NO:12)

**12.3.1.1 Kappa Chain DNA**

CCACTCTCCC	TGCCCCTCAC	CCTTGGACAG	CCGGCCTCCA	TCTCCTGCAG	50
GTCTAGTCAA	AGCCTCGTAT	ACAGTGATGG	AAACACCTAC	TTGAATTGGT	100
TTCAGCAGAG	GCCAGGCCAA	TCTCCAAGGC	GCCTAATTTA	TAAGGTTTCT	150
AACTGGGACT	CTGGGGTCCC	AGACAGATTC	AGCGGCAGTG	GGTCAGGCAC	200
TGATTTCACA	CTGAAAATCA	GCAGGGTGGA	GGCTGAGGAT	GTTGGGGTTT	250
ATTACTGCAT	GCAAGGTTCA	CACTGGCCTC	CGACGTTTCGG	CCAAGGGACC	300
AAGGTGGA	TCAAACGAAC	TGTGGCTGCA	CCATCTGTCT	TCATCTTCCC	350
GCCATCTGAT	GAGCAGTTGA	AATCTGGAAC	TGCCTCTGTT	GTGTGCCTGC	400
TGAATAACTT	CTATCCCAC				419

(SEQ ID NO:51)

**12.3.1.1 Kappa Chain Protein**

PLSLPVTLGQ	PASISCRSSQ	SLVYSDGNTY	LNWFQQRPGQ	SPRRLIYKVS	50
NWDSGVPDRF	SGSGSGTDFT	LKISRVEAED	VGYYCMQGS	HWPPTFGQGT	100
KVEIKRTVAA	PSVFIFPPSD	EQLKSGTASV	VCLLNNFYP		139

(SEQ ID NO:25)

**Figure 1M****12.9.1.1 Heavy Chain DNA**

GTCCAGCCTG	GGAGGTCCCT	GAGACTCTCC	TGTGCAGCGT	CTGGATTCAC	50
CTTCAGTAAC	TATGCCATGC	ACTGGGTCCG	CCAGGCTCCA	GGCAAGGGGC	100
TGGAGTGGGT	GGTAGTTATT	TGGCATGATG	GAAATAATAA	ATACTATGCA	150
GAGTCCGTGA	AGGGCCGATT	CACCATCTCC	AGAGACAATT	CCAAGAACAC	200
GCTGTATCTG	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTATATT	250
ACTGTGCGAG	AGATCAGGGC	ACTGGCTGGT	ACGGAGGCTT	TGACTTCTGG	300
GGCCAGGGAA	CCCTGGTCAC	CGTCTCCTCA	GCCTCCACCA	AGGGCCCATC	350
GGTCTTCCCC	CTGGCGCCCT	GCTCCAGGAG	CACCTCCGAG	AGCACAGCGG	400
CCCTGGGCTG	CCTGGTCAAG	GACTACTTCC	CCGAACCGGT	GACGGTGTCTG	450
TGGAACCTCAG	GCGCTCTGAC	CAGCGGCGTG	CACACCTTCC		490

(SEQ ID NO:39)

**12.9.1.1 Heavy Chain Protein**

VQPGRSLRLS	CAASGFTFSN	YAMHWVRQAP	GKGLEWVVVI	WHDGNNKYIA	50
ESVKGRFTIS	RDNSKNTLYL	QMNSLRAEDT	AVYYCARDQG	TGWYGGFDFW	100
GQGTLVTVSS	ASTKGPSVFP	LAPCSRSTSE	STAALGCLVK	DYFPEPVTVS	150
WNSGALTSGV	HTF				163

(SEQ ID NO:13)

**12.9.1.1 Kappa Chain DNA**

CCTGGAGAGC	CGGCTTCCAT	CTCTTGCAGG	TCTAGTCAGA	GCCTCCTGCA	50
TAGTAATGGA	TACAACTATT	TGGATTGGTA	CCTGCAGAAG	CCAGGACAGT	100
CTCCACAGCT	CCTGATCTAT	TTGGGTTCTA	ATCGGGCCTC	CGGGGTCCCT	150
GACAGGTTCA	GTGGCAGTGG	ATCAGGCACA	GATTTTACAC	TGAAACTCAG	200
CAGAGTGGAG	GCTGAGGATG	TTGGGGTTTA	TTACTGCATG	CAAGCTCTAC	250
AAACTCCTCT	CACTTTCGGC	GGAGGGACCA	AGGTGGAGAT	CAAACGAACT	300
GTGGCTGCAC	CATCTGTCTT	CATCTTCCCG	CCATCTGATG	AGCAGTTGAA	350
ATCTGGAAC	GCCTCTGTTG	TGTGCCTGCT	GAATAACTTC	TATCCCAGAR	400
AGGCCAAAGT	ACATTCCAT				419

(SEQ ID NO:52)

**12.9.1.1 Kappa Chain Protein**

PGEPASISCR	SSQSLLHSNG	YNYLDWYLQK	PGQSPQLLIY	LGSNRASGVP	50
DRFSGSGSGT	DFTLKLRSVE	AEDVGVIYCM	QALQTPITFG	GGTKVEIKRT	100
VAAPSVFIFP	PSDEQLKSGT	ASVVCLLNNF	YPR		133

(SEQ ID NO:26)



**Figure 2A**

CDR	DP5 0	3.1.1	4.1.1	4.8.1	4.10. 2	4.13. 1	4.14. 3	6.1.1	11.2. 1	11.6. 1	11.7. 1	12.3. 1.1	12.9. 1.1
								G					
	G	G	G	G	G			G	G	G		G	
	V	V	V	V	V			V	V	V	V	V	
	V	V	V	V	V			V	V	V	V	V	V
	Q	Q	Q	Q	Q			E	Q	Q	Q	Q	Q
	P	P	P	P	P	P	P	P	P	P	P	P	P
	G	G	G	G	G	G	G	G	G	G	G	G	G
	R	R	R	R	R	R	R	R	R	R	R	R	R
	S	S	S	S	S	S	S	S	S	S	S	S	S
	L	L	L	L	L	L	L	L	L	L	L	L	L
	R	R	R	R	R	R	R	R	R	R	R	R	R
	L	L	L	L	L	L	L	L	L	L	L	L	L
	S	S	S	S	S	S	S	S	S	S	S	S	S
	C	C	C	C	C	C	C	C	C	C	C	C	C
	A	A	V	T	V	A	A	T	A	A	A	A	A
	A	A	A	A	A	A	A	A	A	A	A	A	A
	S	S	S	S	S	S	S	S	S	S	S	S	S
	G	G	G	G	G	G	G	G	G	G	G	G	G
	F	F	F	F	F	F	F	F	F	F	F	F	F
	T	T	T	T	I	T	T	T	T	T	T	T	T
	F	F	F	F	F	F	F	F	F	F	F	F	F
CDR1	S	S	S	S	S	S	S	S	S	S	S	S	S
	S	S	S	N	S	S	S	S	S	S	S	S	N
	Y	Y	H	Y	H	H	H	Y	Y	Y	C	Y	Y
	G	G	G	G	G	G	G	G	G	G	G	G	A
	M	M	M	M	I	I	I	M	M	M	M	V	M
	H	H	H	H	H	H	H	H	H	H	H	H	H
	W	W	W	W	W	W	W	W	W	W	W	W	W
	V	V	V	V	V	V	V	V	V	V	V	V	V
	R	R	R	R	R	R	R	R	R	R	R	R	R
	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q
	A	A	A	A	A	A	A	A	A	A	A	A	A
	P	P	P	P	P	P	P	P	P	P	P	P	P
	G	G	G	G	G	G	G	G	G	G	G	G	G
	K	K	K	K	K	K	K	K	K	K	K	K	K
	G	G	G	G	G	G	G	G	G	G	G	G	G
	L	L	L	L	L	L	L	L	L	L	L	L	L
	E	E	E	E	E	E	E	E	E	E	E	E	E
	W	W	W	W	W	W	W	W	W	W	W	W	W
	V	V	V	V	V	V	V	V	V	V	V	V	V
	A	A	A	A	A	A	A	A	A	A	A	A	V
	V	V	V	V	V	V	V	V	V	V	V	V	V
	I	I	I	I	I	I	I	I	I	I	I	I	I
	W	W	W	W	W	W	W	W	W	W	W	W	W
	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	S	Y	H
	D	D	D	D	D	D	D	D	D	D	D	D	D
	G	G	G	G	G	G	G	G	G	G	G	G	G
CDR2	S	S	R	S	R	R	R	S	S	S	S	S	N

**Figure 2B**

CDR	DP5 0	3.1.1	4.1.1	4.8.1	4.10. 2	4.13. 1	4.14. 3	6.1.1	11.2. 1	11.6. 1	11.7. 1	12.3. 1.1	12.9. 1.1
	N	N	N	N	N	N	N	N	N	H	H	N	N
	K	K	K	K	K	K	K	K	K	K	K	K	K
	Y	Y	Y	H	D	D	D	H	Y	Y	Y	Y	Y
	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	A	A	A	G	A	A	A	A	A	A	A	A	A
	D	D	D	D	D	D	D	D	D	D	D	D	E
	S	S	S	S	S	S	S	S	S	S	S	S	S
	V	V	V	V	V	V	V	A	V	V	V	V	V
	K	K	K	K	K	K	K	K	K	K	K	K	K
	G	G	G	G	G	G	G	G	G	G	G	G	G
	R	R	R	R	R	R	R	R	R	R	R	R	R
	F	F	F	F	F	F	F	F	F	F	F	F	F
	T	T	T	T	T	T	T	T	T	T	T	T	T
	I	I	I	I	I	I	I	I	I	I	I	I	I
	S	S	S	S	S	S	S	S	S	S	S	S	S
	R	R	R	S	R	R	R	R	R	R	R	R	R
	D	D	D	D	D	D	D	D	D	D	D	D	D
	N	N	N	N	N	N	N	N	N	N	N	N	N
	S	S	S	S	S	S	S	S	S	S	S	S	S
	K	K	K	K	K	K	K	K	K	K	K	K	K
	N	N	N	N	N	N	K	N	N	N	N	S	N
	T	T	T	T	T	T	T	T	T	T	T	T	T
	L	L	L	L	L	L	L	L	L	L	L	L	L
	Y	Y	F	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	L	L	L	L	L	L	L	L	L	L	L	L	L
	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q
	M	M	M	M	M	M	M	M	M	M	M	M	M
	N	N	N	N	N	N	N	N	N	N	N	N	N
	S	S	S	S	S	S	S	S	S	S	S	S	S
	L	L	L	L	L	L	L	L	L	L	L	L	L
	R	R	R	R	R	R	R	R	R	R	R	R	R
	A	A	A	A	A	A	A	A	A	A	A	A	A
	E	E	E	E	E	E	E	E	E	E	E	E	E
	D	D	D	D	D	D	D	D	D	D	D	D	D
	T	T	T	T	T	T	T	T	T	T	T	T	T
	A	A	A	A	A	A	A	A	A	A	A	A	A
	V	V	V	V	V	V	V	V	V	V	V	V	V
	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	C	C	C	C	C	C	C	C	C	C	C	C	C
	A	A	A	A	A	A	A	A	A	A	A	A	A
	R	R	R	R	R	R	R	R	R	R	R	R	R
		G	G	G	V	V	V	A	D	G	G	D	D
		A	G	E	A	A	A	G	P	A	T	S	Q
		R	H	R	P	P	P	L	R	V	M	Y	G
		I	F	L	L	L	L	L	G	V	I	Y	T
CDR3		I	G	G	G	G	G	G	A	V	V	D	G

Figure 2C

CDR	DP5 0	3.1.1	4.1.1	4.8.1	4.10. 2	4.13. 1	4.14. 3	6.1.1	11.2. 1	11.6. 1	11.7. 1	12.3. 1.1	12.9. 1.1
		T	P	S	P	P	P	Y	T	P	V	F	W
		P	F	Y	L	L	L	F	L	A	G	W	Y
		C	D	F	D	D	D	D	Y	A	T	S	G
		M	Y	D	Y	Y	Y	Y	Y	M	L	G	G
		D	W	Y	W	W	W	W	Y	D	D	R	F
		V	G	W	G	G	G	G	Y	V	Y	G	D
		W	Q	G	Q	Q	Q	Q	Y	W	W	G	F
		G	G	Q	G	G	G	G	G	G	G	M	W
		Q	T	G	T	T	T	T	M	Q	Q	D	G
		G	L	T	L	L	L	L	D	G	G	V	Q
		T	V	L	V	V	V	V	V	T	T	W	G
		T	T	V	T	T	T	T	W	T	L	G	T
		V	V	T	V	V	V	V	G	V	V	Q	L
		T	S	V	S	S	S	S	Q	T	T	G	V
		V	S	S	S	S	S	S	G	V	V	T	T
		S	A	S	A	A	A	A	T	S	S	T	V
		S	S	A	S	S	S	S	T	S	S	V	S
		A	T	S	T	T	T	T	V	A	A	T	S
		S	K	T	K	K	K	K	T	S	S	V	A
		T	G	K	G	G	G	G	V	T	T	S	S
		K	P	G	P	P	P	P	S	K	K	S	T
		G	S	P	S	S	S	S	S	G	G	A	K
		P	V	S	V	V	V	V	A	P	P	S	G
		S	F	V	F	F	F	F	S	S	S	T	P
		V	P	F	P	P	P	P	T	V	V	K	S
		F	L	P	L	L	L	L	K	F	F	G	V
		P	A	L	A	A	A	A	G	P	P	P	F
		L	P	A	P	P	P	P	P	L	L	S	P
		A	C	P	C	C	C	C	S	A	A	V	L
		P	S	C	S	S	S	S	V	P	P	F	A
		C	R	S	R	R	R	R	F	C	C	P	P
		S	S	R	S	S	S	S	P	S	S	L	C
		R	T	S	T	T	T	T	L	R	R	A	S
		S	S	T	S	S	S	S	A	S	S	P	R
		T	E	S	E	E	E	E	P	T	T	C	S
		S	S	E	S	S	S	S	C	S	S	S	T
		E	T	S	T	T	T	T	S	E	E	R	S
		S	A	T	A	A	A	A	R	S	S	S	E
		T	A	A	A	A	A	A	S	T	T	T	S
		A	L	A	L	L	L	L	T	A	A	S	T
		A	G	L	G	G	G	G	S	A	A	E	A
		L	C	G	C	C	C	C	E	L	L	S	A
		G	L	C	L	L	L	L	S	G	G	T	L
		C	V	L	V	V	V		T	C	C	A	G
		L	K	V	K	K	K		A	L	L	A	C
		V	D	K	D	D	D		A	V	V	L	L
		K	Y	D	Y	Y	Y		L	K	K	G	V
		D	F	Y	F	F	F		G	D	D	C	K
		Y	P	F	P	P	P		C	Y	Y	L	D

*Figure 2D*

[illegible]

# Figure 3

## DP-65 or 4-31 gene product

VSGGSISSGGYYWSWTRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVTISVDTSKNQFSCLKSSVTAADTAVYYCAR  
CDR1 CDR2

## 2.1.3 Heavy Chain Protein

SGPGLVKPSQILSLTCTVSGGSISGGHYWSWTRQHPGKLEWIGYIYYIGNTYYNPSLKSRVTISVDTSKNQFSCLKSSVTAADTAVYYCAR  
CDR1 CDR2  
DSGDYYGIDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ  
CDR3

## Figure 4

### A27 Gene Product

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGSPP  
 CDR1 CDR2 CDR3

### 4.1.1 Kappa Chain Protein

QSPGTLSPGERATLSCRASQSISSSELAWYQQRPQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGTSPWT  
 CDR1 CDR2 CDR3  
 FGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK

### 4.8.1 Kappa Chain Protein

QSPGTLSPGERATLSCRITSMVSSSYLAWYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGISPET  
 CDR1 CDR2 CDR3  
 FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 4.14.3 Kappa Chain Protein

GTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGRSPET  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 6.1.1 Kappa Chain Protein

QSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGISPET  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 4.10.2 Kappa Chain Protein

SPGTLSPGERATLSCRASQSISSSELAWYQQKPGQAPRLIYRPSSRATGIPDSFSGSGGTDFLTISRLEPEDFALYYCQOYGTSPET  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 4.13.1 Kappa Chain Protein

QSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGRSPET  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKGG

## Figure 5

### 012 Gene Product

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFRSGSGTDFTLTISLQPEDFATYYCQQQSYSTP  
 CDR1 CDR2 CDR3

### 3.1.1 Kappa Chain Protein

QSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNFIATSILOSGVPSRFRSGSGTNFTLTINSLHPEDFATYYCQQQSYSTP  
 CDR1 CDR2 CDR3

FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG

### 11.2.1 Kappa Chain Protein

PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFRSGSGTDFTLTISLQPEDFATYYCQQQSYSTP  
 CDR1 CDR2 CDR3

FGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV

### 11.6.1 Kappa Chain Protein

TQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFRSGSGTDFTLTISLQPEDFATYYCQQQSYSTP  
 CDR1 CDR2 CDR3

FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN

### 11.7.1 Kappa Chain Protein

TQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPRVLIAASSLQSGVPSRFRSGSGTDFTLTISLQPEDFATYYCQQQSYSTP  
 CDR1 CDR2 CDR3

FGPGTRVDIERTVAAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAY

## Figure 6

### A10/A26 Gene Product

ENVLTQSPDFQSVTPKEKVTITCRASQSIGSSSLHWYQQKPDQSPKLLIKYASQSESGVPSRFSGSGGTDFTLTINSLEAEDAATYYCHQSSSLPQ  
CDR1 CDR2 CDR3

### 2.1.3 Kappa Chain Protein

SPDFQSVTPKEKVTITCRASQSIGSSSLHWYQQKPDQSPKLLIKYASQSESGVPSRFSGSGGTDFTLTINSLEAEDAATYYCHQSSSLPLT  
CDR1 CDR2 CDR3  
FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE



## Figure 7

### A17 Gene Product

DVVM~~MTQSP~~SLPVTLGQ~~PASISCRSSQSLVYSDGNIT~~YLNWFQ~~QRPQGQSPRRLIYKVSNRDS~~GV~~PDRFSGSGGTDFTLKISRVEAEDVGVYYCMQ~~GTHWP  
CDR1 CDR2 CDR3

### 12.3.1 Kappa Chain Protein

PLSLPVTLGQ~~PASISCRSSQSLVYSDGNIT~~YLNWFQ~~QRPQGQSPRRLIYKVSNRWDS~~GV~~PDRFSGSGGTDFTLKISRVEAEDVGVYYCMQ~~GSHWPP  
CDR1 CDR2 CDR3  
FGQGTKVEIKRTVAAPS~~VFI~~PPSDEQLKSGTASVWCLLNFP

## Figure 8

### A3/A19 Gene Product

DIVMTQSPILSLPVTGPASISCRSSQSLHSNGYNLYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGGTFTLKISRVEAEDVGVYYCMQALQITP  
CDR1 CDR2 CDR3

### 12.2.1 Kappa Chain Protein

PGEPASISCRSSQSLHSNGYNLYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGGTFTLKISRVEAEDVGVYYCMQALQITLT  
CDR1 CDR2 CDR3  
FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP

**Figure 9** Amino-terminal amino acid sequence analysis

Hybridoma	Light chain	MW
CT2.1.3	ND	ND
CT3.1.1	NH <sub>2</sub> -DIQMTQSPSSLSASVGDRVT	26,119
CT4.1.1	NH <sub>2</sub> -EIVLTQSPGTLSPGERAT	23,917
CT4.8.1	NH <sub>2</sub> -EIVLTQSPGTLSPGERAT	23,617
CT4.9.1	NH <sub>2</sub> -DIQMTQSPSSVSASVGDRVT	23,702
CT4.10.2	NH <sub>2</sub> -TGEFVLTQSPGTLSPGER (60%) NH <sub>2</sub> -EFVLTQSPGTLSPGERAT (40%)	24,101
CT4.14.3	NH <sub>2</sub> -EIVLTQSPGTLSPGERAT	23,770
CT4.13.1	NH <sub>2</sub> -EIVLTQSPGTLSPGERAT	23,802
CT6.1.1	NH <sub>2</sub> -EIVLTQSPGTLSPGERAT	23,747

Hybridoma	Heavy chain	MW
CT2.1.3	ND	ND
CT3.1.1	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~80%) NH <sub>2</sub> -PEVQF...(minor sequence~20%)	51,813
CT4.1.1	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~65%) NH <sub>2</sub> -PEVQFNWYVD...(minor sequence~35%)	51,502
CT4.8.1	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPG(R)SL... (major sequence~60%) NH <sub>2</sub> -PEVQFNWY...(minor sequence~40%)	51,597
CT4.9.1	NH <sub>2</sub> -EVQLLESGGGLVQPGGSLRL (free amino terminus)	51,437
CT4.10.2	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~60%) NH <sub>2</sub> -PEVQFNWYVD...(minor sequence~40%)	51,502
CT4.14.3	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSL(R)(L)(S) (major sequence~65%) NH <sub>2</sub> -PEVQFNWYV...(minor sequence~35%)	51,293
CT4.13.1	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~75%) NH <sub>2</sub> -PEVQFN...(minor sequence~25%)	51,305
CT6.1.1	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVEPGRSLRLS* (major sequence~65%) NH <sub>2</sub> -PEVQFNWYVD... (minor sequence~35%)	51,476

\* This heavy chain sequence is similar to the other blocked heavy chain sequences except for a unique Gln->Glu change at position 13.

Figure 10A

antibody	Conc. (mg/ml) (Ec1.58)		IEF	SDS-PAGE		SEC	reported MALDI		n-term. seq. (lc)*	
	reported	observed		(+) b-me	(-) b-me		Hc	Lc	reported	observed
CT 3.1.1	1.1	1.57	smear	50 & 28 kDa	6 bands	139,400	51,813	26,119	DIQMTQSP (SEQ ID NO: 141)	DIQMTQSP (SEQ ID NO: 141)
CT 4.1.1	1.54	1.65	smear	50 & 24 kDa	6 bands	79,900	51,502	23,917	EIVLTQSP (SEQ ID NO: 142)	EIVLTQSP (SEQ ID NO: 142)
CT 4.8.1	1.52	1.54	4 bands	50 & 24 kDa	6 bands	110,300	51,597	23,617	EIVLTQSP (SEQ ID NO: 143)	EIVLTQSP (SEQ ID NO: 143)
CT 4.10.2	1.29	1.77	4 bands	50 & 25 kDa	6 bands	107,200	51,502	24,101	**	***
CT 4.14.3	1.75	1.65	smear	50 & 24 kDa	6 bands	82,800	51,293	23,770	EIVLTQSP (SEQ ID NO: 146)	EIVLTQSP (SEQ ID NO: 146)
CT 6.1.1	1.36	1.3	4 bands	50 & 24 kDa	6 bands	101,100	51,476	23,747	EIVLTQSP (SEQ ID NO: 147)	EIVLTQSP (SEQ ID NO: 147)
* all heavy chains n-terminally blocked (not sequenced in-house)										
** mixed sequence reported: TGEFVLTQSP (60) (SEQ ID NO: 144) & EFVLTQSP (40) (SEQ ID NO: 145)										
*** mixed sequence observed TGEFVLTQSP (60) (SEQ ID NO: 144) & EFVLTQSP (40) (SEQ ID NO: 145)										

$IOD_{280nm} = 0.633 \text{ mg/ml}$   
 Ec-1.58

Figure 10B

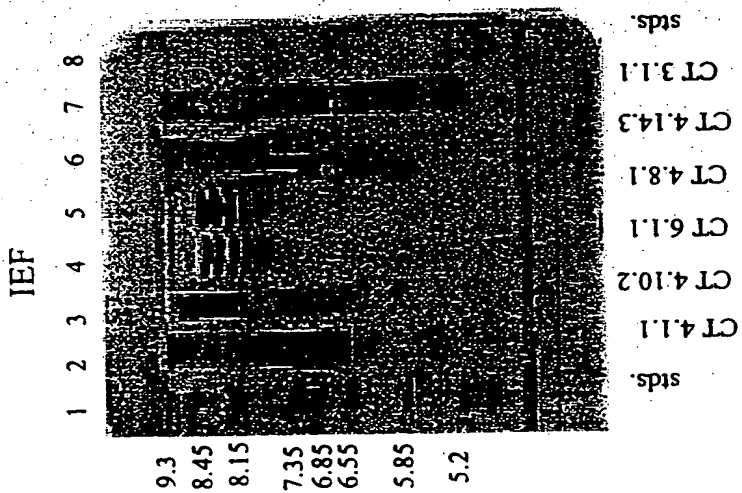


Figure 10C

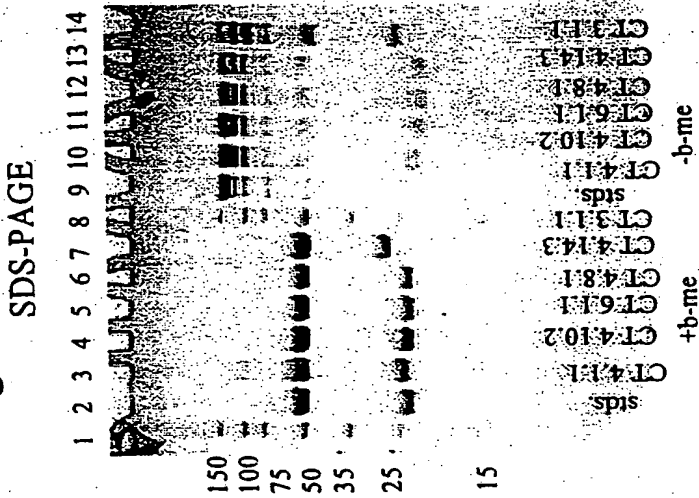
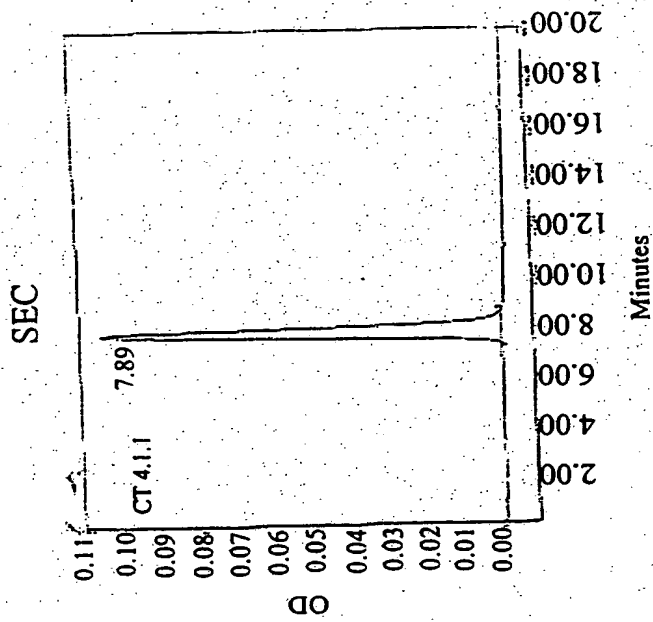
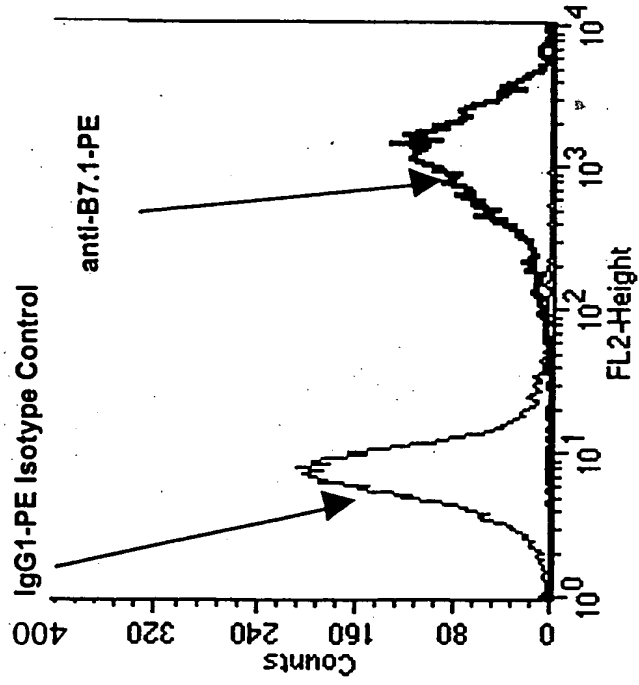


Figure 10D



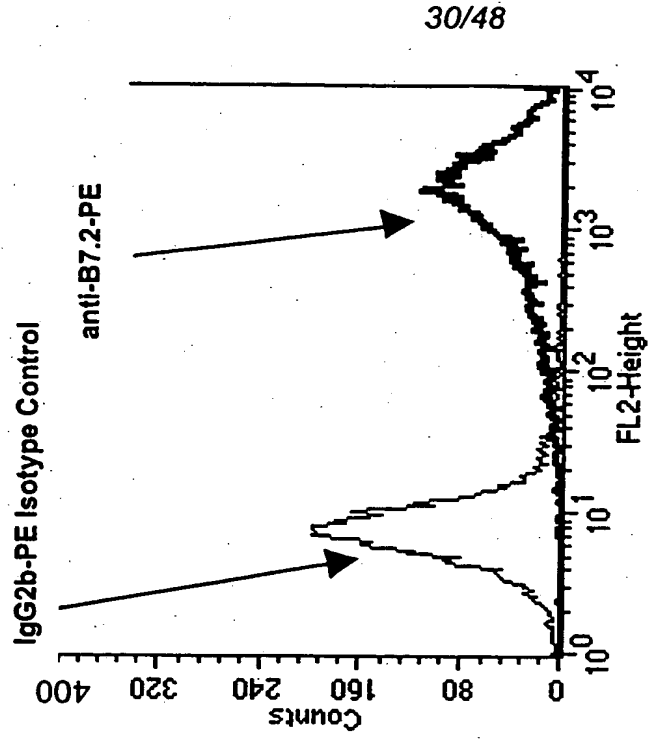
**Figure 11A**



99.7% B7.1 pos.

Expression of B7.1 and B7.2 on Raji Cells

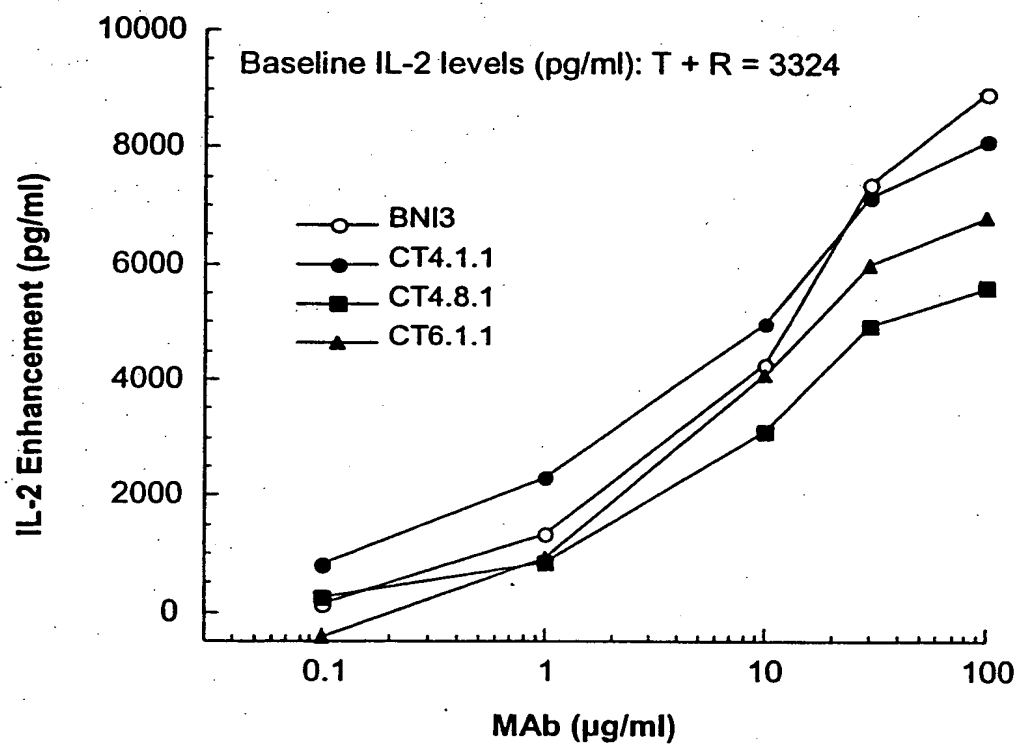
**Figure 11B**



99.7% B7.2 pos.

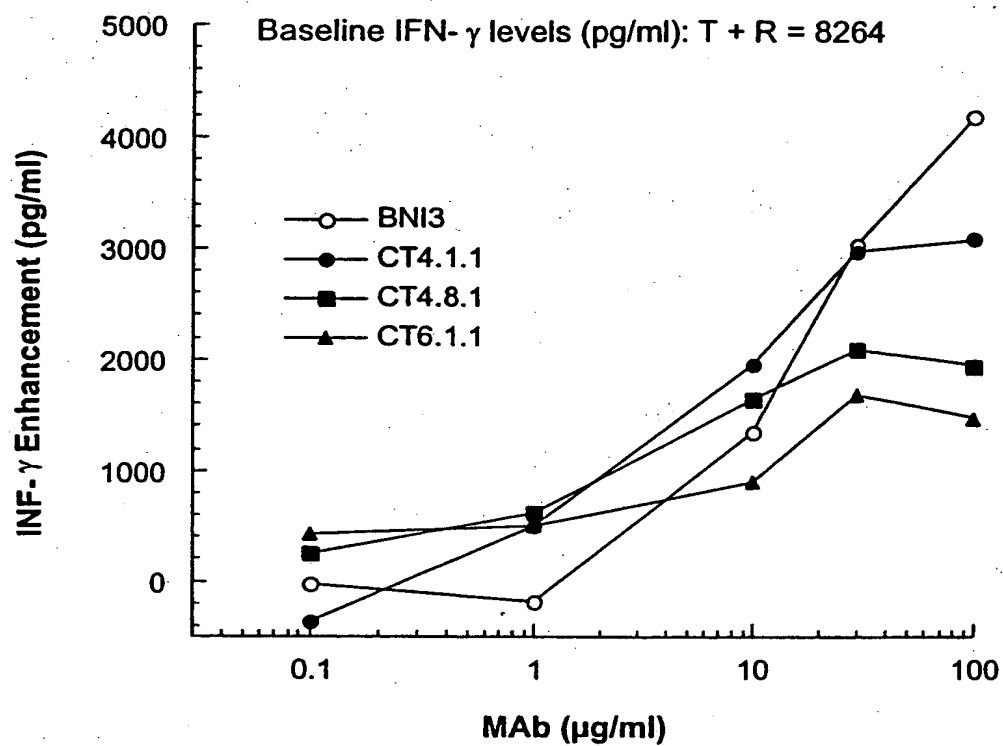
**Figure 12**

**Enhancement of Human T Cell IL-2 Production  
Induced by Anti-CTLA4 XenoMouse MAbs in  
the 72 Hour T Blast / Raji Assay**



**Figure 13**

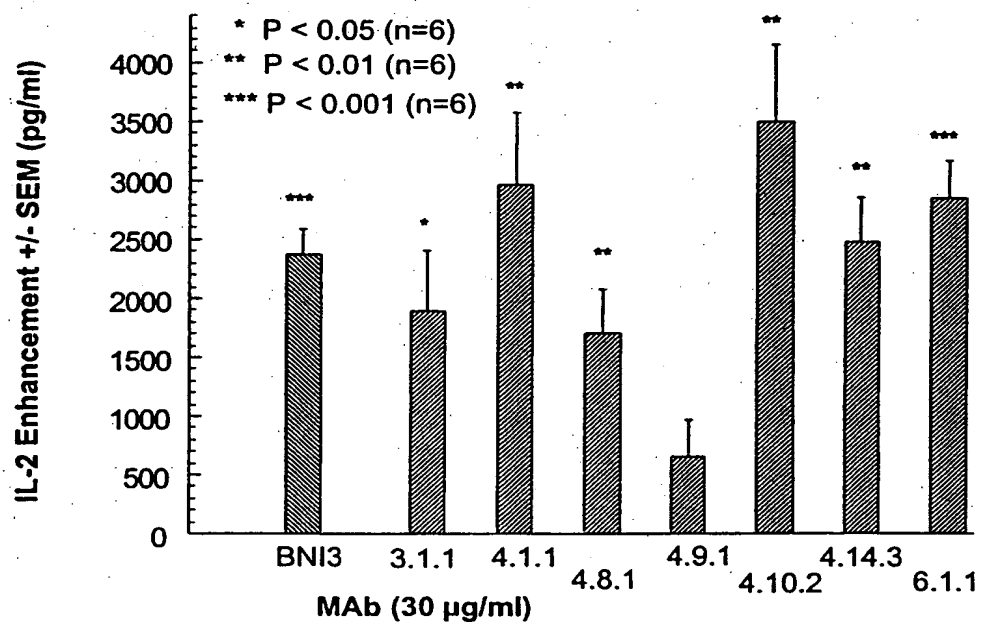
**Enhancement of Human T Cell IFN- $\gamma$  Production  
Induced by Anti-CTLA4 XenoMouse MAbs in  
the 72 Hour T Blast / Raji Assay**





**Figure 14****Enhancement of Human T Cell IL-2 Production  
Induced by Anti-CTLA4 XenoMouse MAbs in  
the 72 Hour T Blast / Raji Assay (6 Donors)**

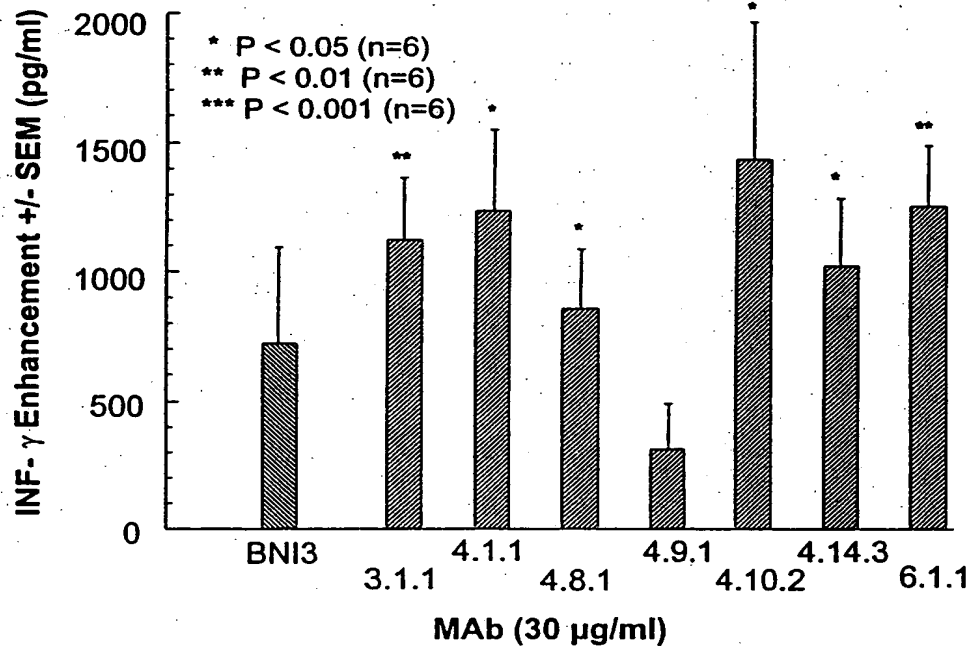
Baseline IL-2 levels (pg/ml): T + R = 9187, T + R + IgG2a = 9389, T + R + IgG2 = 8509



**Figure 15**

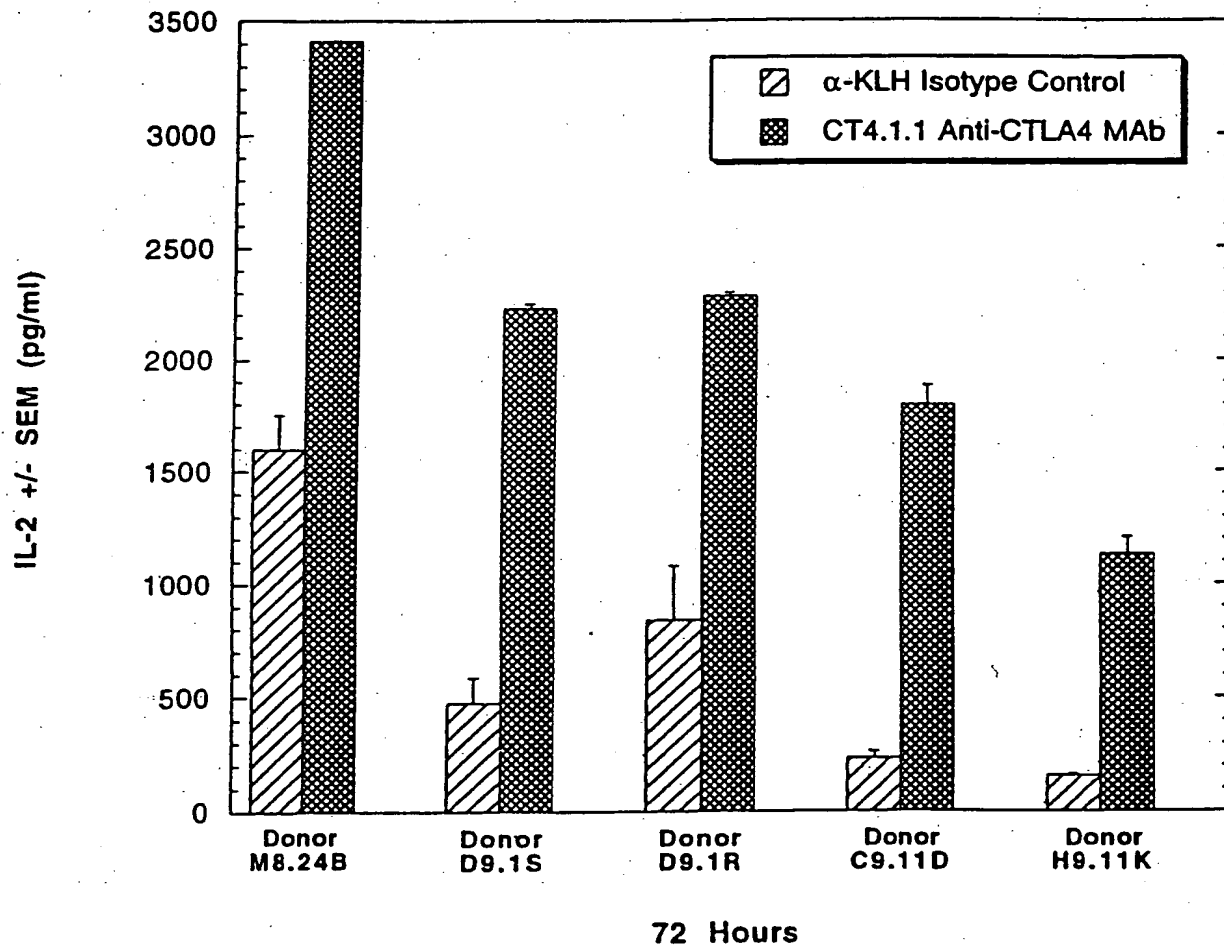
**Enhancement of Human T Cell IFN- $\gamma$  Production  
Induced by Anti-CTLA4 XenoMouse MAbs in  
the 72 Hour T Blast / Raji Assay (6 Donors)**

Baseline IFN- $\gamma$  levels (pg/ml): T + R = 4780, T + R + IgG2a = 4868, T + R + IgG2 = 4331



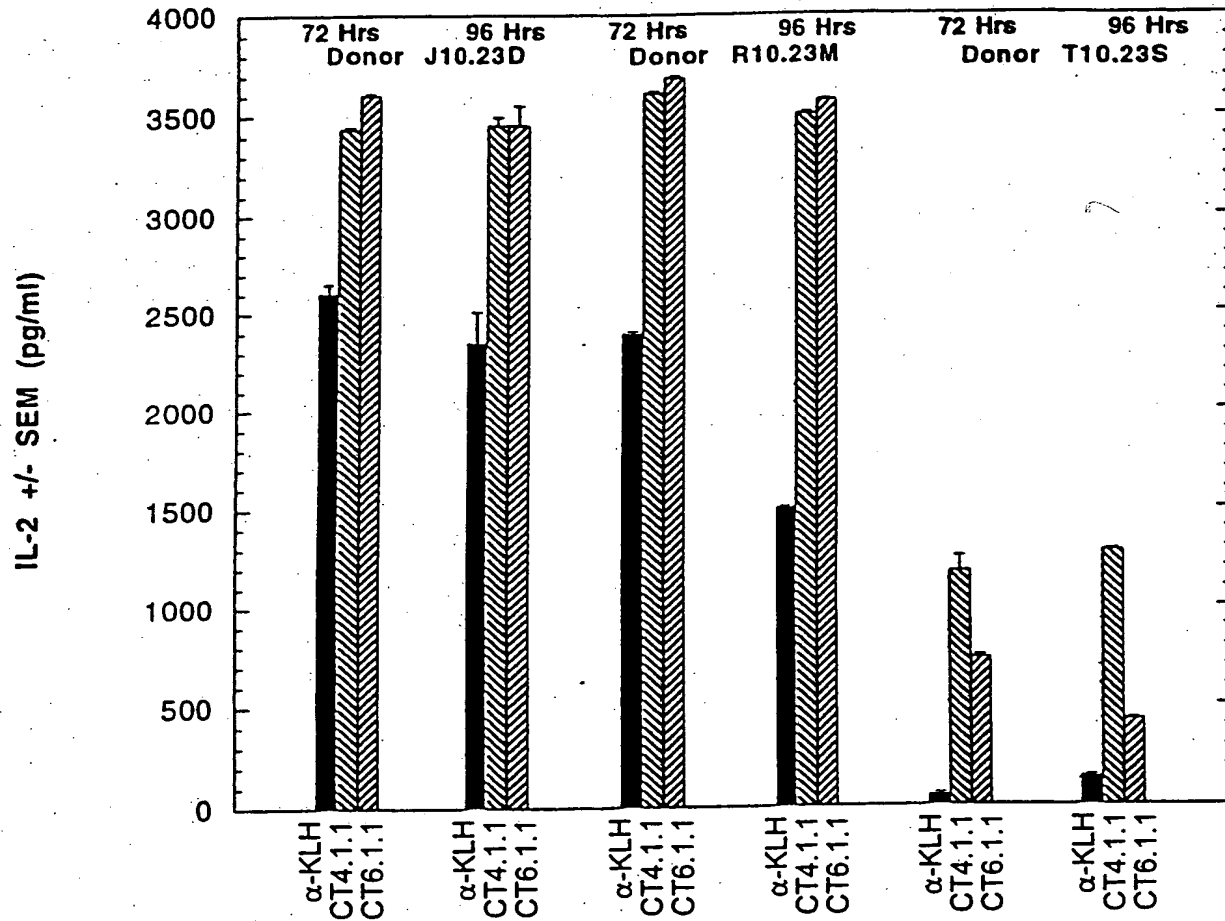
**Figure 16**

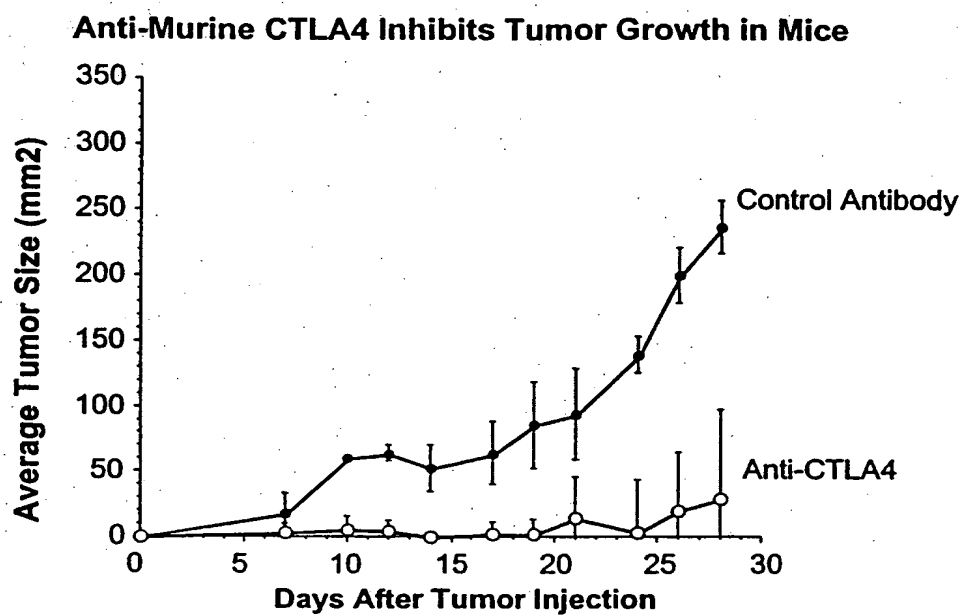
**Enhancement of IL-2 Production Induced by Anti-CTLA4 MAb CT4.1.1 (30  $\mu$ g/ml) Binding to Human PBMC Stimulated with SEA (100 ng/ml) Plus Anti-CD3 MAb (60 ng/ml)**



**Figure 17**

**Enhancement of IL-2 Production Induced by Anti-CTLA4 MAbs  
(30  $\mu$ g/ml) in Human Whole Blood Stimulated with SEA  
(100 ng/ml) Plus Anti-CD3 MAb (60 ng/ml)**

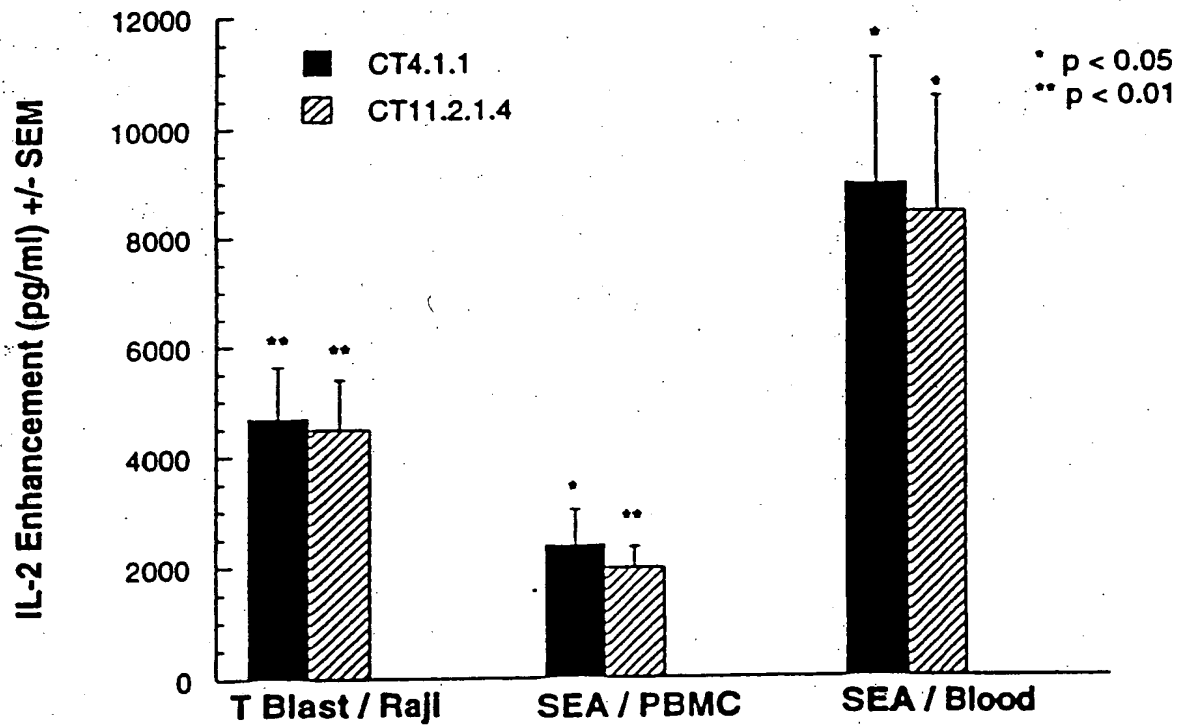


**Figure 18**

Treatment was administered on day  
0,4,7,and 14 after tumor challenge

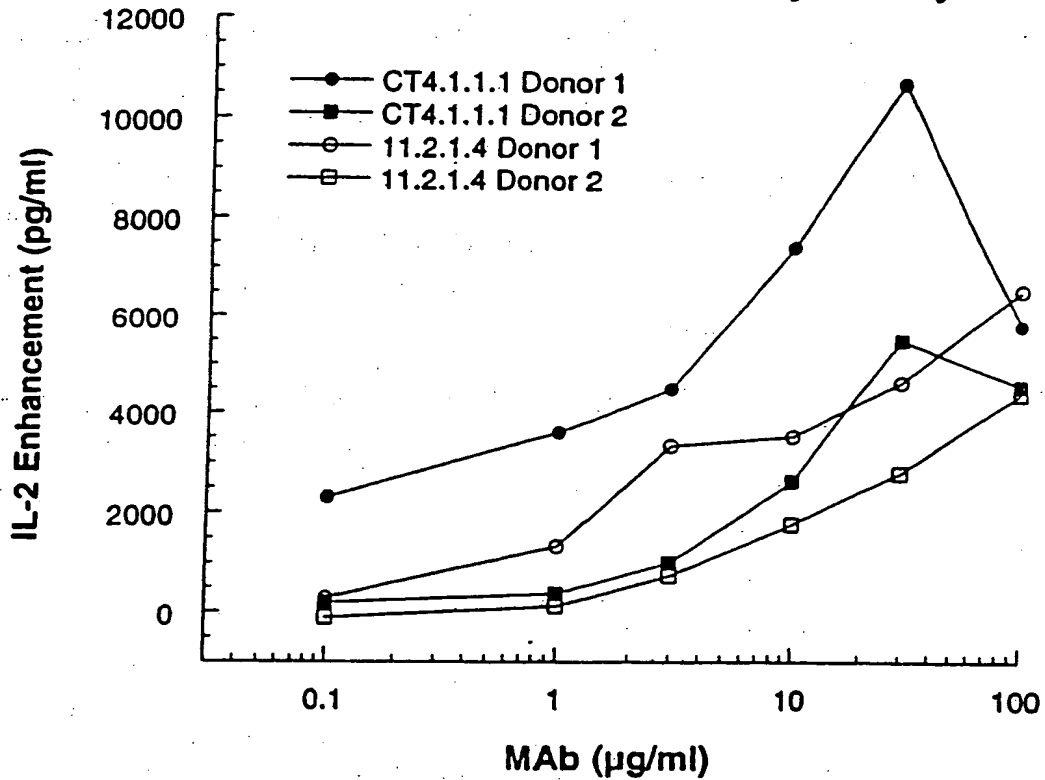
**Figure 19**

**Enhancement of IL-2 Production Induced by Anti-CTLA4 MAbs  
(30  $\mu$ g/ml) in the 72 Hour T Blast / Raji and  
Superantigen Assays (6 Donors)**



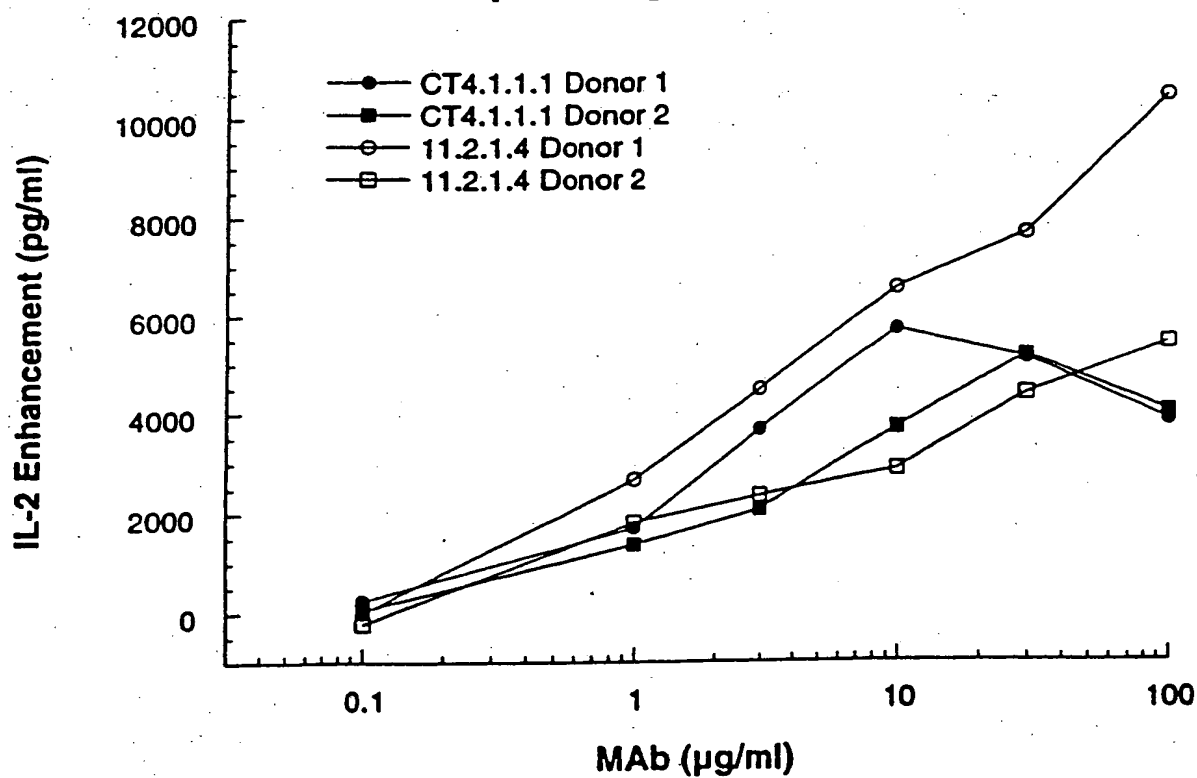
**Figure 20**

**Enhancement of Human T Cell IL-2 Production  
Induced by Anti-CTLA4 MAbs in  
the 72 Hour T Blast / Raji Assay**



**Figure 21**

**Enhancement of IL-2 Production Induced by Anti-CTLA4  
MAbs in Whole Blood Stimulated with  
Superantigen (100 ng/ml)**





- Signal peptides shown in bold and large text
- Open reading frame for genomic clone underlined
- Mutations introduced to make deglycosylated Ab (N294Q) double underlined and large text

**Figure 22A** 4.1.1 IgG2 Heavy Chain cDNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTACCTTCAGTAG  
CCATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC  
CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA  
CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGTCACT  
TCGGTCTTTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCAGCC  
TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
TGACGGTGTCTGGAAGTCAAGCGCTCTGACCAGCGGCGTGCACACCTTCCCA  
GCTGTCTTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA  
GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTGCGAGTGCCCA  
CCGTGCCCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAA  
ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACAGTGCGTGGTGG  
TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC  
GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCAC  
GTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCA  
AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCAGCCCCCATCGAGAAA  
ACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC  
CCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA  
AAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG  
GAGAACAACACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTT  
CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT  
TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  
CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:53)

**Figure 22B** 4.1.1 IgG2 Heavy Chain Genomic DNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTACCTTCAGTAG  
 CCATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC  
 CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTCACT  
 TCGGTCTTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCT  
 AGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
 CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
 TGACGGTGTCTGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA  
 GCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
 CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA  
 GCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGG  
 GTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTG  
 CAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGG  
 CCTCTGCCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC  
 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCCCTACCCAGGCCCTTCACACACA  
 GGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGC  
 CCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGTCTGGAC  
 ACCTTCTCTCCTCCAGATCCGAGTAACCTCCCAATCTTCTCTCTGCAGAGCGC  
 AAATGTTGTGTCGAGTGCCCCACCGTGCCCCAGGTAAGCCAGGCCAGGCCTCGCC  
 CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGG  
 CCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCTCAGCACCACTGT  
 GGCAGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGA  
 TCTCCCGGACCCCTGAGGTACGTGCGTGGTGGTGGACGTGAGCCACGAAGAC  
 CCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAA  
 GACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCC  
 TCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTC  
 TCCAACAAAGGCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGG  
 TGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCACCC  
 TCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCG  
 AGAACCACAGGTGTACACCTGCCCCCATCCCGGGAGGAGATGACCAAGAACC  
 AGGTACGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCGTG  
 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACACCTCCCAT  
 GCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGA  
 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTG  
 CACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ  
 ID NO:54)

**Figure 22C** 4.1.1 IgG2 Heavy Chain Protein

**MEFGLSWVFLVALLRGVQC**QVQLVESGGGVVQPGRSRLRLSCVASGFTFSS  
 HGMHWVRQAPGKLEWVAVIWDGRNKYYADSVKGRFTISRDNKNTLFLQMN  
 SLRAEDTAVYYCARGGHFGPFDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTS  
 ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP  
 SSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCPAPPVAGPSVFLFPPK  
 PKDTLMI SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST  
 FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLF  
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSGDSFF  
 LYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK (SEQ ID  
 NO:63)

**Figure 22D** 4.1.1 IgG2 Heavy Chain cDNA N294Q

ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGTTGCTCTTTTAAGA  
 GGTGTCCAGTGT CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTACCTTCAGTAG  
 CCATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC  
 CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTCACT  
 TCGGTCTTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC  
 TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
 CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
 TGACGGTGTCTGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGACACCTTCCCA  
 GCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
 CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA  
 GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTGCGAGTGCCCA  
 CCGTGCCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCTAAA  
 ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGG  
 TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC  
 GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCCAAGCAC  
 GTTCCGTGTGGTCAAGCTCTCACCGTTGTGCACCAGGACTGGCTGAACGGCA  
 AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCAGCCCCCATCGAGAAA  
 ACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC  
 CCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCA  
 AAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG  
 GAGAACAACCTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTT  
 CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT  
 TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  
 CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:55)

**Figure 22E** 4.1.1 IgG2 Heavy Chain Protein N294Q

MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGRSLRLSCVASGFTFSS  
 HGMHWVRQAPGKGLEWVAWIYDGRNKYYADSVKGRFTISRDN SKNTLFLQMN  
 SLRAEDTAVYYCARGGHFGPFDYWGGTLTVTVSSASTKGPSVFPLAPCSRSTS  
 ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP  
 SSNFGTQTYTCNV DHKPSNTKVDKTV ERKCCVECPPCPAPPVAGPSVFLFPPK  
 PKDTLMISRTP EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFQST  
 FRVVS VLT VVH QDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL P  
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFF  
 LYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
 NO:64)

**Figure 22F** 4.1.1 Kappa Chain DNA

**ATGGAAACCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC**  
**CCAGATAACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC**  
 TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTATTA  
 GCAGCAGCTTCTTAGCCTGGTACCAGCAGAGACCTGGCCAGGCTCCCAGGCTC  
 CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAAGTGG  
 CAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAG  
 ATTTTGCAGTGTATTACTGTCAGCAGTATGGTACCTCACCCCTGGACGTTCCGGC  
 CAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT  
 CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCC  
 TGCTGAATAACTTCTATCCCAGAGAGGGCCAAAGTACAGTGAAGGTGGATAAC  
 GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA  
 CAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGA  
 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTC  
 ACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:56)

**Figure 22G** 4.1.1 Kappa Chain Protein

**METPAQLLFLLLLWLPLDTTGEIVLTQSPGTLSSLSPGERATLSCRASQSI**  
 SSFLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED  
 FAVYYCQQYGTSPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCL  
 LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLTLSKADYEK  
 HKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:65)

**Figure 22H** 4.8.1 Heavy Chain DNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTACAGCGTCTGGATTACCTTCAGTAA  
 CTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGTAATAAAACACTATGGAGACTCCGTGAAGGGC  
 CGATTCACCATCTCCAGTGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGAGAGAC  
 TGGGGTCTCTACTTTGACTACTGGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  
 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCAC  
 CTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAAC  
 CGGTGACGGTGTCTGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGCACACCTTC  
 CCAGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGT  
 GCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGC  
 CCAGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTGCGAGTGC  
 CCACCGTGGCCAGCACCACTGTGGCAGGACCGTCAGTCTTCTCTTCCCCC  
 AAAACCCCAAGGACACCCCTCATGATCTCCCCGACCCCTGAGGTACAGTGCCTGG  
 TGGTGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGAC  
 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAG  
 CACGTTCCGTGTGGTCAGCGTCTCACCCTTGTGCACCAGGACTGGCTGAACG  
 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCAGCCCCCATCGAG  
 AAAACCATCTCCAAAACCAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT  
 GCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGG  
 TCAAAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG  
 CCGGAGAACAACACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTT  
 CTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG  
 TCTTCTCTACGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG  
 AGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:57)

**Figure 22I** 4.8.1 Heavy Chain Protein

**MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGRSLRLSCTASGFTFSN**  
**YGMHWVRQAPGKGLEWVAVIWDGSKHYGDSVKGRFTISSDNSKNTLYLQMN**  
**SLRAEDTAVYYCARGERLGSYFDYWGQGLTVTVSSASTKGPSVFPLAPCSRST**  
**SESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV**  
**PSSNFGTQTYTCNVDPKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPP**  
**KPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS**  
**TFRVSVSLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL**  
**PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSF**  
**FLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID**  
**NO:66)**

**Figure 22J** 4.8.1 Kappa Chain DNA

**ATGGAAACCCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC**  
**CCAGATACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC**  
**TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGACCAGTGTTAGCAGCA**  
**GTTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC**  
**TATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGG**  
**GTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTG**  
**CAGTCTATTACTGTCAGCAGTATGGCATCTCACCCTTCACTTTCGGCGGAGGG**  
**ACCAAGGTGGAGATCAAGCGAACTGTGGCTGCACCATCTGTCTTCATCTTCCC**  
**GCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGA**  
**ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTC**  
**CAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAC**  
**CTACAGCCTCAGCAGCACCTTGACGCTGAGCAAAGCAGACTACGAGAAACACA**  
**AAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG**  
**AGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:58)**

**Figure 22K** 4.8.1 Kappa Chain Protein

**METPAQLLFLLLLWLPDTTGEIVLTQSPGTLSSLSPGERATLSCRTSVSSS**  
**YLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA**  
**VYYCQQYGISPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN**  
**NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHK**  
**VYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:67)**

**Figure 22L** 6.1.1 Heavy Chain DNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCTGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTTCGAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTACAGCGTCTGGATTACCTTCAGTAG  
 TTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGCAATAAACACTATGCAGACTCCGCGAAGGGC  
 CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGAAGTGC  
 TGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC  
 TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
 CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
 TGACGGTGTTCGTGGAAGTCAAGCGCTCTGACCAGCGGCGTGCACACCTTCCCA  
 GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
 CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA  
 GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTTCGAGTGCCCA  
 CCGTGCCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCTAAA  
 ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACAGTGCCTGGTGG  
 TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC  
 GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCAC  
 GTTCCGTGTGGTCAGCGTCTCACCCTGTGTGCACCAGGACTGGCTGAACGGCA  
 AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAA  
 ACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTTGCC  
 CCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCA  
 AAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG  
 GAGAACAACACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTT  
 CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT  
 TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  
 CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:59)

**Figure 22M** 6.1.1 Heavy Chain Protein

**MEFGLSWVFLVALLRGVQC**QVQLVESGGGVVEPGRSLRLSCTASGFTFSS  
 YGMHWVRQAPGKGLEWVAVIWDGNSNKHYSADSAKGRFTISRDNSTNTLYLQMN  
 SLRAEDTAVYYCARAGLLGYFDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTS  
 ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP  
 SSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPEPPAPPVAGPSVFLFPPK  
 PKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST  
 FRVVSIVLTQVHLDWLNQKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL  
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSGDSFF  
 LYSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID  
 NO:68)

*Figure 22N* 6.1.1 Kappa Chain DNA

**ATGGAAACCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC**  
**CCAGATAACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC**  
 TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGTAGGGCCAGTCAAAGTGTTA  
 GCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCAGGCCCTC  
 ATCTATGGTGTATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAG  
 TGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATT  
 TTGCAGTGTATTACTGTCAGCAGTATGGTATCTCACCATTCACTTTTCGGCCCT  
 GGGACCAAAGTGGATATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTT  
 CCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGC  
 TGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCC  
 CTCCAATCGGGTAACTCCCAGGAGAGTGTACACAGAGCAGGACAGCAAGGACAG  
 CACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAAC  
 ACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACA  
 AAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:60)

*Figure 22O* 6.1.1 Kappa Chain Protein

**METPAQLLFLLLLWLPLDTTGEIVLTQSPGTLSPGERATLSCRASQSVS**  
 SYLAWYQQKPGQAPRPLIYGVSSRATGIPDRFSGSGSGTDFTLTISRLEPEDF  
 AVYYCQQYGISPFITFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL  
 NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKH  
 KVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:69)

*Figure 22P* 11.2.1 IgG2 Heavy Chain DNA:

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAG  
 CTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC  
 CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCGAGGG  
 GAGCTACCCTTTACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACC  
 ACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC  
 GCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCA  
 AGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGGCGCTCTGACC  
 AGCGGCGTGCACACCTTCCCAGCTGTCTTACAGTCTCAGGACTCTACTCCCT  
 CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCT  
 GCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGC  
 AAATGTTGTGTCGAGTGCCCAACCGTGCCCAAGCACCACTGTGGCAGGACCGTC  
 AGTCTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCC  
 CTGAGGTACAGTGCGTGGTGGTGACGTGAGCCACGAAGACCCGAGGTCCAG  
 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG  
 GGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAAGCTCCTACCGTTGTGC  
 ACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGC  
 CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAGGGGCAGCCCCGAGA  
 ACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGG  
 TCAGCCTGACCTGCCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCGTGGAG  
 TGGGAGAGCAATGGGACGCGGAGAACTACAAGACCACACCTCCCATGCT  
 GGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA  
 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC  
 AACCCTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID  
 NO:61)

**Figure 22Q** 11.2.1 IgG2 Heavy Chain Protein:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY  
 DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPRGATLY  
 YYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFP  
 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDH  
 KPSNTKVKDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTC  
 VVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVS VLT TVVHQDWL  
 NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTC  
 LVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQG  
 NVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:70)

**Figure 22R** 11.2.1 IgG2 Kappa Chain DNA:

ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTACTC  
 TGGCTCCGAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCCT  
 CCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAG  
 AGCATTAACAGCTATTTAGATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA  
 ACTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA  
 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT  
 GAAGATTTTGCAACTTACTACTGTCAACAGTATTACAGTACTCCATTCACTTT  
 CGGCCCTGGGACCAAAGTGGAATCAAACGAACTGTGGCTGCACCATCTGTCT  
 TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTG  
 TGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGA  
 TAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA  
 AGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTAC  
 GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC  
 CGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGTGA (SEQ ID NO:62)

**Figure 22S** 11.2.1 IgG2 Kappa Chain Protein:

DIQMTQSPSSLSASVGDRVTITCRASQSINSYLDWYQQKPGKAPKLLIYAASS  
 LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTPFTFGPGTKVEI  
 KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS  
 QESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG  
 EC (SEQ ID NO:71)